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SEARCH REQUEST FORM

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Scientific and Technical Inf rmation Center

	25201		
Requester's Full Name: M.A.h	IALICKA	Examiner # : 7820	Date: Oct 4, 2002
Art Unit: しらくユ Phone !	Number 30 5 - 727	70 Serial Number:	09/720,583
Mail Box and Bldg/Room Location	n: 10 D 0 6 Resu	ılts Format Preferred (cir	cle): PAPER DISK E-MAIL
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f more than one search is subm			
Please provide a detailed statement of the include the elected species or structures, I utility of the invention. Define any terms known. Please attach a copy of the cover	search topic, and describe reywords, synonyms, acron that may have a special me	as specifically as possible the syms, and registry numbers, a eaning. Give examples or rel	subject matter to be searched. and combine with the concept or
Title of Invention:	Promonitor	Pruvels	Lor
The of invention.	Dintar	Dayrel	et al
Inventors (please provide full names):	1000	renwecs	01 00
Earliest Priority Filing Date:	6/25/99		
For Sequence Searches Only Please inclu appropriate serial number.	de all pertinent information ((parent, child, divisional, or issu	ed patent numbers) along with the
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Thank you so	much i	n ordvance	
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			Point of Contact: Toby Port inical Info. Specialist CM1 6A04 703-308-3634
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STAFF USE ONLY	Type of Search	Vendors and co	st where applicable
Searcher:	NA Sequence (#)	STN	
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Searcher Location:	Structure (#)	Questel/Orbit	
Date Searcher Picked Up: 10/4	Bibliographic	Dr.Link	
Date Completed:	Litigation		
Searcher Prep & Review Time:	Fulltext	Sequence Systems	
Clerical Prep Time:	Patent Family	WWW/Internet	

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Online Time: _

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DSM NV (
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Propionibacterium freudenreichii
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Propionibacterineae;
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AX007138
AX007138.1 GI:9995029
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Pouwels, P.H., Jore, J.P.,
Propionibacterium vector
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                                                                                                               EP 0972835-A 1 19-JAN-2000
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273. .1184
                                                                 Location/Qualifiers
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Propionibacteriaceae;
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Result No.

Score

Query Match Length DB

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Description

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Patent: WO 9967356-A 1 29-DEC-1999;
GIST BROCADES BV (NL); JORE JOHANNES PETRUS MARIA (NL);
NICOLE VAN (NL); LUITEN RUDOLF GIJSBERTUS MARIE (NL);
PIETER HENDRIK (NL)
                                                                                                                        Propionibacterium freudenreichii.
Propionibacterium freudenreichii
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Propionibacterineae;
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                                                                                                                                                                                                     CACGAGGTGCGCGCC
                                                                                                                                                                                                            cacgaggtgcgcgcc
2 (bases 1 to 3555)
Jore, J.P.M. and van I
Direct Submission
Submitted (31-JUL-200
                                                                                                                                    AF291751
Propionibacterium f
AF291751
AF291751.1 GI:1095
                                                       Pouwels, P. Efficient
                                                                    Propionibacterium.
1 (bases 1 to 3555)
Jore, J.P., van Luijk, N.,
                                                                                            Propionibacterium freudenreichii.
Propionibacterium freudenreichii
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Propionibacterineae;
                                Appl - Env
21091935
                                       Efficient transformation system freudenreichii based on a novel Appl—Baviron—Microbiel 67 (2)
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freudenreichii
               Luijk, N.
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                                        vector
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plasmid
                                                                     .G.,
                                                       Propionibacterium
                                                                                              Actinobacteridae;
Propionibacteriaceae;
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(31-JUL-2000)

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EIHALPEAGNPRRNVTRSTVGRNVTLFDTTRWAAYRAVHSWGGPVAEWBHTVFEHIH
LLNETILJADEPATGPLGLNELKHLSRSISRWVWRNFTPETFRARQKAISLRGASKGGK
EGGHKGGIASGASRRAHTROOFLEGLS"
05 a 1156 c 1075 g 619 t
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/strain="LMG16545"
/db_xref="taxon:1744"
228. .485
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TVSDFWPPDSWQRTKRKNPVGLGRNCTLFETVWDVYRVCVESGSATWIPRPEDRHDL
KORSSICARRVTEFSEALPASELRATIRSFYKWITTRYTGWLDSRTTSEEKSAAYHRN
TGRQGGLKGGTASAKLAARPPASALWRQSAMATRERIFVMG"
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1298. .2251
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17. . . 283
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17. .283
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Appl. Environ
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Propionibacterium acidi-propionici
complete sequence.
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Yamashita, M. and Murooka, Y.
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Bacteria; Firmicutes; Actinobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (E-mail:murooka@res.bio.eng.osaka-u.ac.jp, Fax:81-6-879-7418)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murooka,Y., Hashimoto,Y.,
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Propionibacterium jensenii plasmid
ORF6 and ORF7, ORF8, ORF9 and PpnA.
AJ250233
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Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Propionibacterineae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Propionicin SM1, a bacteriocin from Propionibacterium isolation and characterization of the protein and its Syst. Appl. Microbiol. 23 (2), 174-184 (2000)
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PpnA gene; theta replicase.
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s., Stierli, M.P.,
                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:1749"
                                                                                                                                                                                                                                                                                                                                                                  /isolate="Raw Milk"
                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Propionibacterium
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                                                                                                            note="ORF10"
                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                            note="ORF8"
                                                                                                                                                                                                                                                                                                                                                                                   /strain="DF1"
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Institute of Food
ch, SWITZERLAND
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Pred. No. 8.1e-11;
0; Mismatches 273;
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Moore,M.W., Bowling,D. and Glenn,D.
Nucleotide sequence of a plasmid from Brevibacterium linens:
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Moore, M.W., Glenn, D. and Bowling, D.
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                                                                                                                                                                                                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(3951. .3956)
4034. .4996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3052. .3591)
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a 2349 c 2133 g 1555 t 2 others
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	cccaetttgaacaegecgaggaatggaccaegetgaacgtgaetegeatgetteaetgca 269 	Qy 210 Db 3971	a b
6;	y Match 3.2%; Score 112.6; DB 1; Length 7610; Local Similarity 46.9%; Pred. No. 7.3e-10; hes 595; Conservative 0; Mismatches 629; Indels 45; Gaps	Query Match Best Local Matches 59	

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                                                                                                                                                                                                                                                                                                                                          Submitted (11-OCT-2000) Biodegradation Genetics Laboratory, Institute of Genetics and Selection of Industrial Microorga 1st Dorozhny Pr., 1, Moscow 113545, Russia
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Ryabchenko, L.E., Nov
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rqlatihtpromprrpdravglgrnvimfdatrrwaypowwqhrngtgrdwdhlylqh
                                                                                                                                                            rhodochrous pRC4 putative replication protein (repA), Rhodococcus rhodochrous pKA22 putative theta replicase (ORF2), Rhodococcus erythropolis pFAJ2600 putative replication protein (repA), Mycobacterium fortuitum pAL5000 putative replication protein (37K)"
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                                                                                                                                                                                                                                      putative; similar to putative Rhodococcus
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                                                              GCTTGTTTGCTGAGCCGCGTGACGATTACCTCGGCCGTGCGAAAGCTCGCCGTGACAAAG
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Rhodococcus rl
(repB)"
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/db_xref="GI:11095366"
/tanslation="MGGKNPVRRKMTAAAAAEKFGASTRTIQRLFAEPRDDYLGRAK
ARRDKAVELRKQGLKYREIAEAMELSTGIVGRLLHDARRHGEISAEDLSA"
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49.2%;
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Pred. No. 6.1e-07;
0; Mismatches 402;
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No. 6.1e-07;
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Submitted (14-MAR-2000) Kenji Maruhashi, Petroleum Energy Center,
Bio-Refining Process Laboratory; Sodeshi-cho 1900, Shimizu,
Shizuoka 424-0037, Japan (E-mail:k.maru@brpl.pecj.or.jp,
Tel:+81-543-67-9550, Pax:+81-543-67-9552)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB040101.1 GI:7262572
DNA-binding replication
Rhodococcus rhodochrous
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AB040101
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Rhodococcus
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Ishii,Y., Hirasawa,K. and Maruhashi,K.
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/gene="repA"
/1142. .2062
/gene="repA"
/note="putative
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2052. .:
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a 828 c 755 g 475 t
                                                                                                                                                                                                                                                                                              /translation="MDMSGGSLSGDWEQLWLPLWPLATDDLLLGVYRMPRODALDRRY LEANPQALSNLLVYDVDHDDAALRALSAAGNHPLPNAIVENFTHE RTEYARRKPLAYAAAVNEGLRALVGDDAAYSGLMTKNPTHSAWDTHWIHAETRSLDDLEHDLGHMMPPFWRQSKRRREDDVGLGRNCMLFETARTWAYRELRCHWGDDEGLGKAI QVEAADLNAAFSEPLFVSEVRAIAASIHRWIVTKSRWMADGPAVYEATFVAIQSARGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similar to putative theta replicase from Rhodococcus rhodochrous pKA22 and RepA proteins from Mycobacterium fortuitum pAL5000 and related plasmids."
                                                                                                                                                  similar to putative DNA-binding replication Rhodococcus erythropolis pFAJ2600"
                                                                                                                                                                                                                                                                                KMTEKKREANRRRATKYDRDLVRKEATDGS'
                                                                                                                                                                                                                                                                                                                                                                                          /product="replication
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/db_xref="GI:7262573"
                                                       /product="DNA-binding replication
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/db_xref="GI:7262574"
                                                                                                                                                                                                     /gene="repB"
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/transl_table=11
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1. .2582
                                                                                                                 /transl_table=11
                                                                                                                                                                                      /note="putative
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rhodochrous plasmid p
protein, DNA-binding
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                                                                       Corynebacterium glutamicum Plasmid 36 (1), 36-41 (1996)
                                                                                                             Ankri,S., Bouvier,I., Reyes,O., A Brevibacterium linens pRBL1 r
                                                                                                                                                                                                     Brevibacterium linens
Brevibacterium linens
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                                               TCATGCGCGCCATGTGGAAATCGAAAAGCCTGGCAACCCCAACGCCGTAGTCGAGAACCCTG
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Submitted (02-NOV-1995) Serge Ankri, Centre National de la
Recherche Scientifique, Institut de Genetique Moleculaire (URA
1354) Universite Paris-Sud Batiment 409, Piece 206, Orsay, 91405,
France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="aab03568.1"
/db_xref="GI:1079742"
/translation="MSTASTETWGOMWLPLWPLASDDLLOGIYRTSRHNALELRYIEA
/translation="MSTASTETWGOMWLPLWPLASDDLLOGIYRTSRHNALELRYIEA
RPQSLSNLLVVDIDHPDALMRAMWNKAWQPNAVVENPANGHAHAVWALAEPVTRTEY
ARRKPLAYAAAVTEGLRRSUDGDKGYSGLITKNPTHDQWEASWLTDHLYNLDELTEHL
TVSDFWPPDSWQRTKRKNPVGLGRNCTLFETVRWDVYRVARTIRKRNEHPTPEDRHDL
EAAIVNLCQGMNSTESEALPASEIRATIRSFYKWITTRYTGWLDSRTTSQSKSAAYHR
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Submitted (04-AUG-1995) Jose A. Ainsa, Dep
Biologia Molecular, Facultad de Medicina,
y Cantabria, Zaragoza/Santander, Spain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ainsa,J.A., Martin,C., Cabeza,M., De la Cruz,F. and Mendiola,M.V. Construction of a family of Mycobacterium/Escharichia coll shuttl vectors derived from pAL5000 and pACYC184: their use for cloning antibiotic-resistance gene from Mycobacterium fortuitum Gene 176 (1-2), 23-26 (1996)
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1 (bases 1 to 5252)
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Cloning vector pSUM36
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                                                                                     /gene="lacz"
/codon_start=1
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                                                                                                                                                                                                      /db_xref="taxon:42470"
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/db_xref="GI:993048"
                                                                                                                                                                            1099. .1269
/gene="lacz"
                                                                                                                                                                                                                                                 /organism="Cloning vector pSU36"
/note="GenBank Accession Number
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/db_xref="taxon:42459"
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translation="SLALAVVLQRRDWENPGVTQLNRLAAHPPFASWRNSEEARTDRP/
                                                                                                                                                                                                                                                                                                                                          note="Mycobacterium"
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/db_xref="GI:993049"
/db_xref="GI:993049"
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                                                                                                       Sequence
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Stover, C.K.
Bacterial expression vectors containing
signals of lipoproteins
patent: US 5583038-A 1 10_DEC-1996;
Bacterial expression vectors signals of lipoproteins
                        1 (bases 1 to
Stover, C.K.
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Pred. No. 0.000
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I31863
                                            Bacterial expression vectors containing signals of lipoproteins Patent: US 5583038-A 20 10-DEC-1996; Location/Qualifiers
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Stover,C.K.
Bacterial expression vectors containing signals of lipoproteins
Patent: US 5583038-A 21 10-DEC-1996;
Location/Qualifiers
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AAT28276	AAT28273	AAT28272	AAQ21502	AAT64413	AAV69312	AAV69313	AAZ49691	ID	
Plasmid pMV261 seq	Plasmid pMH29 sequ	Plasmid pMY200. S	Vector pMV206 for	plasmid pMV101. S	M. fortuitum plasm	M. fortuitum plasm	Propionibacterium	Description	

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ALIGNMENTS

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RESULT
AAZ49691
ID AAZ4
Propionibacterium LMG 16545; vector; plasmid; antigen; vaccine; enzyme; nutritional factor; growth factor; clotting factor; antimicrobial; drug hormone; vitamin B12; animal feed; lactic acid bacteria; foodstuff;
                                                                                                                                                                                                                                                                                 Propionibacterium plasmid LMG 16545 DNA.
                                                                                                                                                                                                                                                                                                       07-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                          AAZ49691 standard; DNA; 3555 BP
25-JUN-1999;
                        29-DEC-1999.
                                               WO9967356-A2
                                                                                                                                                                                             Propionibacterium freudenreichii LMG 16545.
                                                                                                                                                                                                                     cheese; cyclic; circular; ds.
99WO-EP04416
                                                                                                       /product= "Propionibacterium LMG 16545 protein-1"
/note= "Encoded by ORF-1"
1181..1438
                                                                                                                                                          Location/Qualifiers
273..1184
                                                                     /product= "Propionibacterium LMG 16545 protein-2"
/note= "Encoded by ORF-2"
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Query Match
Best Local Similarity
Matches 3555; Conserv
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Origin of replication; vaccine; cytotoxic Tlymphocyte; treatmer intracellular pathogen; allergy; macrophage; immunogen; adjuvant;

vaccine; cellular immunity; Th-1 cell; cancer; treatment; prevention; disease; autoimmune; allergy; bovine spongiform encephalitis; BSE; adjuvant; ds.

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Mycobacterium

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CC plasmid pAL 5000 origin of replication, ori which has been derived by PCR analysis. This sequence is used in a method which results in the CC formation of Mycobacterium recombinant vaccines from compositions that CC provide a continuous source of protein to an animal and stimulate CC cellular immunity. Such compositions are used to stimulate cellular CC immunity (by inducing Th-1 cells or cytotoxic T lymphocytes), CC particularly as vaccines (live or dead) for treating and preventing CC diseases caused by intracellular pathogens (bacteria, viruses, rickettsia CC or protozoa), and also cancer, autoimmune diseases, allergy and bovine CC administered by injection, orally and nasally. These compositions provide consistent and long-lasting immunity. Transformed cells used in the CC method are retained within macrophages, blocking the killing mechanism CC but producing protective immunogen which is processed and presented by the macrophage. Several immunogens may be included in the same vaccine and the Mycobacterium cells serve as adduvant.
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Best Local S
Matches 274
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Pred. No. 3.9e-10;
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Query Match

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                                        This genomic DNA sequence contains is the Mycobacterium fortiutum CC plasmid pAL 5000 origin of replication, ori. This sequence is used in a CC method which results in the formation of Mycobacterium recombinant CC vaccines from compositions that provide a continuous source of protein to CC an animal and stimulate cellular immunity. Such compositions are used to Stimulate cellular immunity. Such compositions are used to CC stimulate cellular immunity for or dead) for treating and CC preventing diseases caused by intracellular pathogens (bacteria, viruses, CC rickettsia or protozoa), and also cancer, autoimmune diseases, allergy CC and bovine spongiform encephalitis, in humans or animals. The vaccines CC provide consistent and long-lasting immunity. Transformed cells used in CC provide consistent and long-lasting immunity. Transformed cells used in CC provide consistent and protective immunogen which is processed and CC presented by the macrophages. Several immunogens may be included in the CC came vaccine and the Murcharderium cells carve as additionart
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term cellular immunity - useful against intracellular pathogens,
cancer and autoimmune disease, and are retained in host macropha
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Best Local Similarity 47.8%; Matches 274; Conservative

Pred. No. 4e-1 0; Mismatches

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Matches 274
                                                                                                                                                                                                                                                                             This sequence represents the plasmid pMV101. This plasmid was used in the construction of a series of vectors used to produce the recombinant Mycobacteria of the invention. The recombinant mycobacteria of the invention are transformed with DNA encoding a polypeptide which comprises a lipoprotein secretion signal sequence and an antigen (Ag) heterologous to the mycobacteria. The lipoprotein secretion signal causes the Ag to be produced as a lipoprotein. The mycobacteria may be used in the form of a live bacterial vaccines against Lyme disease, where the bacteria express a surface protein of Borrelia burgdorferi, the causative agent of Lyme disease.
                                                                                                                                              2852
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P-PSDB; AAW14834-36.
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                 tgccttcaccgtcctacgtgtccatg-----aaccgtgtcacgaccaccggacacatcg
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                                                ACCTGCTGGTCGTGGACGTAGACCATCCAGACGCAGCGCTCCGAGCGCTCAGCGCCCGGG
                                                               ccttggtcatcaccgatcgagatgcttcggatgctgactgggccgcagacctcgctgggc
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3221..3860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vector pMV206 for cloning genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ21502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTACACACTCAGCCACATCGAGGCCGAGCTCGGCGCGAACATGCCACCGCCGCGCTGGC
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/note- "kanamycin ı
1220..2011
                          91WO-US04833
                                                                                                                                                                                                                                                                                                        /note- "M.rep cassette"
3925..4016
                                                                                                                                                                                                                                                                                                                                                                                       2026..3924
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "E.rep
2012..2025
                                                                                                                                                                                                                                                      /function= Multiple_cloning_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Kanamycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= KanR
                                                                                                                                                                                                                                                                                                                                                                                                             note-
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                                                                                                                                                                                                                                                                                                                                                                                                             "MluI-NotI linker"
                                                                                                                                                                         "contains 16 unique restriction sites, stop codons in all 3 reading frames a a transcription terminator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cassette'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in E.coli and mycobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resistance
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                                                                                                                                                                                                      frames and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cassettes of all the components necessary for plasmid replication in E.coli and mycobacteria (E.rep and M.rep, respectively) and for selection of transformants (KanR) were constructed using the PCR technique. A multiple cloning site was synthesised. The cassettes were constructed to allow directional cloning and assembly into a plasmid where all transcription is unidirectional. Plasmid pMV206 was derived from plasmid pMV204 which was made up of all the cassettes. It was modified by the insertion of an Mull-NotI linker between the M.rep and E.rep cassettes to facilitate removal of
                                                                                                                                                                                                                                                                                                                                                                                                                                        2502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA site-specific integration into Mycobacteria - useful as adjuvant in vaccines and as therapeutic agent for malaria, influenza, herpes and human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacobs WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUL-1990;
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Local Similarity 47.6%;
nes 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ep in further constructions. 
 AAQ21568\hbox{-}Q21573 for the PCR primers used in the construction individual cassettes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtcagcagaccacgtacaaagcggctccgacgccgctagggcggaattgcgcactgttcg
                                                                                                                                                                                   accggatcacaaagaacccgctcagcaccgcccatgcgaccctctggggccccgcagacg
                                                                                                                                                                                                                                                    tgctcgcccgcgtcgaggggcctatgcgacgttctcggcggcgatgcatcctacgggc
                                                                                                                                                                                                                                                                                                                     tctatgccttgaagaaccctgtgtgtctgaccgatgccgcgcggcgacggcctatcaacc
                                                                                                                                                                                                                                                                                                                                                                    tgccttcaccgtcctacgtgtccatg-----aaccgtgtcacgaccaccggacacatcg
                                                                                                                                                                                                                                                                                                                                                                                                                                      acctgctggtcgtggacgtagaccatccagacgcagcgctccgagcgctcagcgcccggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccttggtcatcaccgatcgagatgcttcggatgctgactgggccgcagacctcgctgggc 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aaagccgcgcgtcggcctaggccgccggtacatcgaggcgaacccaacagcgctggcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgactcggcagagggcgctggagctgccttacatcgaagcgaacccgttggtcatgcagt 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agctctggctgccgtactggccgctggcaagcgatctgctcgatggggatctaccgcc
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                                                  cagggaacccgcgtcgcaacgtcacccgatcaacggtcggccgcaacgtcaccctgttcg
                                                                                                                                                                gcctcatgaccaaaaaccccggccacatcgcctgggaaacggaatggctccactcagatc
                                                                                                                                                                                                                                   acatggcggcgtgcgcaaggccttcggcgcgccgtcgatggcgaccgcagttactcag
                                                                                                                                                                                                                                                                                                   tgtgggcactcaacgccctgttccacgcaccgaatacgcgcggcgtaagccgctcgcat 2681
                                                                                              tctacacactcagccacatcgaggccgagctcggcgcgaacatgccaccgccgcgctggc
                                                                                                                               cyctctacgagctgcgcgccctcgcacacaccctcgacgagatccacgcactgccggagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 80.6; DB 13;
Pred. No. 1.3e-09;
0; Mismatches 294;
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RESULT
AAT64421
ID AAT
This sequence represents the plasmid pMV206. This plasmid was used in the construction of a series of vectors used to produce the recombinant Mycobacteria of the invention are transformed with DNA encoding a polypeptide which comprises a lipoprotein secretion signal apolypeptide which comprises a lipoprotein secretion signal
                                                                                                                                                                                                 Mycobacteria expressing secretion signal of lipoprotein and heterologous antigen, esp. outer surface protein A or B of Borr burgdorferi - are used in the form of a live bacterial vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                      Lyme
                             sequence and an antigen (Ag) heterologous to the mycobacteria. The lipoprotein secretion signal causes the Ag to be produced as a lipoprotein. The mycobacteria may be used in the form of a live bacterial vaccines against Lyme disease, where the bacteria express a surface protein of Borrelia burgdorferi, the causative agent of
                                                                                                                                                                Example 1;
                                                                                                                                                                                        against Lyme disease
                                                                                                                                                                                                                                                  WPI; 1997-042315/04.
                                                                                                                                                                                                                                                                           Stover CK;
                                                                                                                                                                                                                                                                                                                       17-NOV-1992;
21-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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                                                                                                                                                                                                                                                                                                 (MEDI-) MEDIMMUNE
                                                                                                                                                                                                                                                                                                                                                            21-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                   10-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pMV101; Mycobacteria; antigen; bacterial vaccine; Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pMV206.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                               Fig 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                       92US-0977630
91US-0780261
                                                                                                                                                                                                                                                                                                                                                            91US-0780261
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "M.rep
3925..4120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "E.rep cassette"
2012..3920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "kan gene"
1220..2011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/note= "NheI/SpeI kan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .21..936
                                                                                                                                                              122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               "Synthetic multiple cloning site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eria; lipoprotein secretion signal
ne; Lyme disease; Borrelia burgdor:
amplify; PCR; polymerase chain rea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
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chain reacti
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Sequence

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03-OCT-1994;

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Best Local Similarity
Matches 273; Conserv
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                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis; Mycobacterium avium;
Mycobacterium intracellulare; Mycobacterium kansasii;
Mycobacterium scrofulaceum; Mycobacterium leprae; tub
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                                                                    02-OCT-1995;
                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pMH28 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT28272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT28272 standard;
                                                                                                                   11-APR-1996
                                                                                                                                                                    WO9610645-A1
                                                                                                                                                                                                                                                                                                                                                                         reporter gene;
                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pMH28; vector; firefly; luciferase;
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                                                                                                                                                                                                                                                                     .eprosy; antibiotic; tuberculostatic; vaccine;
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                                                                                                                                                                                                                                                                                                                                         luminescence; BCG; Mycobacterium bovis; tuberculosis; Mycobacterium avium;
                                                                    95WO-US12642
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1.3e-09;
nes 294;
                                                                                                                                                                                                                                                                                                                                                                                              DNA cassette;
                                                                                                                                                                                                                                                                drug screening;
                                                                                                                                                                                                                                                                                                tuberculosis;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quantification of mycobacteria by luminescence - using treporter strains contg. a lux gene, permits the determn. efficacy of anti-mycobacterial and prophylactic compsns.
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               acaccaccgcatgtgggcataccgggccgtcc
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attccgtcaggttgtgggcctatcgtcccgccc
                                                               gtcagcagaccacgtacaaagcggctccgacgccgctagggcggaattgcgcactgttcg
                                                                                     cagggaacccgcgtcgcaacgtcacccgatcaacggtcggccgcaacgtcaccctgttcg
                                                                                                                                                           gcctcatgaccaaaaaccccggccacatcgcctgggaaacggaatggctccactcagatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is the complete sequence of plasmid pMH28. constructed by inserting a multiple cloning
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                                                                                                                                                                                                                                                                     acatggcggcgtgcgcgaaggccttcggcgcgcgtcgatggcgaccgcagttactcag
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Pred. No. 1.4e-09;
0; Mismatches 294
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                                                                                                                                                                                                                                                                                                         This is the complete sequence of plasmid pMH29. This plasmid has to been constructed by inserting a multiple cloning site and an Escherichia coli TIT2 terminator sequence into plasmid pPA207SC, to based on plasmid pMY206 (AAT28281), to give plasmid pPA207SC) and insertion of a multiple cloning site to give pMH29. A mutant firefly lucliferase (EC-1.13.12.7) reporter gene is inserted to give plasmid pMY30-lux (AAT28278). This type of vector may be used in a new method for quantifying Mycobacterium infection in vivo. An animal is injected with e.g. Mycobacterium bovis BCG, etc., transfected with one of these vectors, and reporter gene expression is detected by luminescence in tissues without lysis or cell concentration. The method may be used to determine the efficacy of antibiotic, tuberculostatic and vaccine compositions.
                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 273; Conserv
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This is the complete sequence of plasmid pMV261. This plasmid an extrachromosomal Mycobacterium-Escherichia coli shuttle expression vector. A mutant FFlux firefly luciferase (EC-1.13. reporter gene DNA cassette may be inserted downstream from a
                                                                                         Quantification of mycobacteria by luminescence reporter strains contg. a lux gene, permits the efficacy of anti-mycobacterial and prophylactic
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Mycobacterium bovis; Mycobacterium tuberculosis; Mycobacterium avium; Mycobacterium intracellulare; Mycobacterium kansasii;

Mycobacterium scrofulaceum; Mycobacterium leprae; tu leprosy; antibiotic; tuberculostatic; vaccine; drug

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the complete sequence of plasmid pMH30-lux. This plasmid has been constructed by inserting a multiple cloning site and an Escherichia coli T1T2 terminator sequence into plasmid pPA207SC, based on plasmid pMY206 (AAT28281), to give plasmid pMH28 (AAT28272) and insertion of a multiple cloning site to give pMH28 (AAT28273). A mutant firefly luciferase (EC-1.13.12.7) reporter gene, with an Ile ATA codon (rare in mycobacteria) changed to ATC to enhance expression, is inserted to give pMY30-lux. The vector is expression, is inserted to give pMY30-lux. The vector is extrachromosomal, and contains a synthetic BCG heat shock protein. hsp70-tac promoter. Although levels of transformants are low, expression levels are very high from the hsp70-tac promoter. This type of vector may be used in a new method for quantifying Mycobacterium bovis BCG, etc., transfected with one of these vectors, and reporter gene expression is detected by luminescence in tissues without lysis or cell concentration. The method may be used to determine the efficacy of antibiotic, tuberculostatic and vaccine
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                                                                                          mycobacteria) changed to ATC to enhance expression, into the extrachromosomal Mycobacterium-Escherichia coli shuttle expression vector plasmid pMy261 (ATC28276), downstream from the BCG heat show protein hsp60 promoter. Although levels of transformants are low, expression levels are high from the hsp60 promoter. This type of vector may be used in a new method for quantifying Mycobacterium infection in vivo. An animal is injected with e.g. Mycobacterium bovis BCG, etc., transfected with of the first procession in the control of these vectors, and
                                                                                                                                                                                                                                                                                                                                        Quantification of mycobacteria by luminescence - using lareporter strains contg. a lux gene, permits the determn. efficacy of anti-mycobacterial and prophylactic compsns.
                                           reporter gene expression is detected by luminescence without lysis or cell concentration. The method may determine the efficacy of antibiotic, tuberculostatic
                                                                                                                                                                                                                                     This is the complete sequence of plasmid pMV261-lux. This plasmid has been constructed by insertion of a mutant firefly luciferase (EC-1.13.12.7) reporter gene, with an Ile ATA codon (rare in
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r gene; luminescence; BCG; hsp60 promoter;
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     03-OCT-1994;
                                                                                                                                                                                                           Synthetic
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Pred. No. 1.5e-09;
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Length

4120;

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This is the complete sequence of plasmid pMV206. This plasmid may the has been used in construction of vectors for use in Mycobacterium to spp. The plasmid may be modified to construct plasmid pPA207SC, to followed by insertion of a multiple cloning site and an Escherichia coli TIT2 terminator sequence, to give plasmid pMH28 (AAT28272) and its derivative plasmid pMH29 (AAT28273). A mutant firefly luciferase (EC-1.13.12.7) reporter gene is inserted to give plasmid pMV30-lux (AAT28278). This type of vector may be used in a new method for quantifying Mycobacterium infection in vivo. An animal is injected with e.g. Mycobacterium bovis BCG, etc., transfected with one of these vectors, and reporter gene expression is detected by luminescence in tissues without lysis or cell concentration. The method may be used to determine the efficacy of
                                                                                                                                                                                                                                                                                                                                                                                                         reporter strains contg. a lux gene, permits the efficacy of anti-mycobacterial and prophylactic
                                                                                                                                                                                                                                                                                                                                                                                                                                                Quantification of mycobacteria by luminescence
Sequence 4120
                                         antibiotic, tuberculostatic and vaccine compositions.
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BP; 921 A; 1126 C; 1166 G; 907 T; 0
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Pred. No. 8.1e
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3.1e-09;
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Matches 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expression vector for expressing protein or polypeptide in mycobacterium - contg DNA sequences encoding lipoprotein secretion signal and peptide heterologous to bacteria expression protein of lipoprotein heterologous to bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytotoxic T-lymphocyte response; transformed Mycobacteria; BCG Mycobacterium smegmatis; vaccine; cell mediated immunity; HIV; pertussis; malaria; influenza virus; CTL; herpes virus.
           2501
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                                                                                                                                                                                                                                                                                                                                              Score 68.6; DB 14;
Pred. No. 1.1e-06;
0; Mismatches 294;
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     2560
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RRESULT 14
ARAC41316/c
ID 4AQ413
XX AAQ413
XX AAQ413
XX CYTOTO
KW CYTOTO
KW MYCODA
XX MYCODA
XX MYCODA
XX KEY
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                             92WO-US09075
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cytotoxic T-lymphocyte response; transformed Mycobacteria; Mycobacterium smegmatis; vaccine; cell mediated immunity; pertussis; malaria; influenza virus; CTL; herpes virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pMV101 - a deletion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgtgggcactcaacgcccctgttccacgcaccgaatacgcgcggcgtaagccgctcgcat 2680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tctatgccttgaagaaccctgtgtgtctgaccgatgccgcgcggcgacggcctatcaacc
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= 6025
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5257..6076
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                                         3220..3862
                                                                                                                                                                                                                                                                                                                                                                      complement (1602..2544)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 version of plasmid pyUB125, which had 792 bases of the tet gene (inactivated by prior manipulations) deleted. The plasmid represents an expression vector. The HSP61 coding sequence was inserted between the NheI and BamHI sites to form pMV65A.

NOTE: When the proteins encoded by this sequence were decoded, the published sequence was found to contain approx. 65 codons which did not code for the amino acids dictated by the universal genetic code. The sequence also contained many insertions and deletions which upset the open reading frame that was displayed as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expression vector for expressing protein or polypeptide in mycobacterium - conty DNA sequences encoding lipoprotein secretion signal and peptide heterologous to bacteria expressing
                                                                                           2434
                                                                                                                                                                                                                                                                                2554
                                                                                                                                                                                                                                                                                                                                                                       2614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoded proteins. The complementary strand was also found to contain many insertions and deletions that did not have corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 5; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stover
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                               cagggaacccgcgtcgcaacgtcacccgatcaacggtcggccacgtcaccctgttcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgccttcaccgtcctacgtgtccat-----gaaccgtgtcacgaccaccggacacatcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccttggtcatcaccgatcgagatgcttcggatgctgactgggccgcagacctcgctgggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tgactcggcagagggcgctggagctgccttacatcgaagcggaacccgttggtcatgcagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agagetggetgceaegeeageeggetggegtcageegagaagtetggggcgtaeegggeaeg 360
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DB; AAR34542; AAR34543; AAR34544.
GTGAGCAGACCAAGTACAAAGCGGCTCCGACGCCGCTAGGGCGGAATTGCGCACTGTTCG
                                                                                                                                                                                  GCCTCATGACCAAAAAACGCCGGCCACATCGCCTGGGAAACGGAATGGGTCCACTCAGATC
                                                                                                                                                                                                                 accggatcacaaagaacccgctcagcaccgcccatgcgaccctctggggccccgcagacg
                                                                                                                                                                                                                                                                           ACATGGCGGCGTGCGCCGAAGGCCTTCGGCGCGCGCGTCGACGGCGACCGCAGTTACTCAG
                                                                                                                                                                                                                                                                                                             tgctcgcccgcgtcgagcagggcctatgcgacgttctcggcggcgatgcatcctacgggc
                                                                                                                                                                                                                                                                                                                                                                     TGTGGGGACTCAACGCCCCTGTTCCACGCACCGAATACGCGCGGGGGTAAGCCGCTCGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTCCCATCCGCTGCCCAACGCGATCGTGGGCAATCGCGCCAACGGCCACACGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAGCCGCGCGTCGGCCCTAGGGCCCCGGTACATCGAGGGGGAACCGAAGAGGGCTGGCAA 2735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCTCTGGCTGCCGTACTGGGCGCTGGCAAGCGACGATCTG-CTCGAGGGGATCTACGCC 2795
                                                                                         cgctctacgagctgcgcgccctcgcacacccctcgacgagatccacgcactgccggagg
                                                                                                                                                                                                                                                                                                                                                                                                              tctatgccttgaagaaccctgtgtgtctgaccgatgccgccgcgcgacggcctatcaacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCTGCTGGTCGTGGACGTAGACCATCCAGACGCAGCGCTCCGAGCGCTCAGCGCCGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein of lipoprotein heterologous to bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           represents that of plasmid pMV101. asmid pYUB125, which had 792 bases (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bases on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0780261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1405 A; 1892 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 68.6; DI
Pred. No. 1.3e
0; Mismatches
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.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294;
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Query Match Best Local Similarity

1.68;

Score Pred.

58.6; DB 13; No. 0.00032;

Length 4811;

Sequence

4811

BP; 1076 A; 1376

C; 1225 G;

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other;

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RESULT 15
AAQ31743/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2314
                           inserted between the NheI and BamHI sites to form pMv65A.

NOTE: When the proteins encoded by this sequence were decoded, the published sequence was found to contain approx. 65 codons which did not code for the amino acids dictated by the universal genetic
                                                                    This sequence represents that of plasmid pMV101. This is a mod version of plasmid pYUB125, which had 792 bases of the tet gen (inactivated by prior manipulations) deleted. The plasmid represents an expression vector. The HSP61 coding sequence was
                                                                                                                                                                                                                                                                                                                                                     cds
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                                                                                                                          Example 1;
                                                                                                                                              transformed Mycobacteria
                                                                                                                                                         Tetanus vaccination -
                                                                                                                                                                                                                      (MEDI-) MEDIMMUNE INC.
                                                                                                                                                                                                                                            06-JUN-1991;
                                                                                                                                                                                                                                                                 01-JUN-1992;
                                                                                                                                                                                                                                                                                      10-DEC-1992
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ALIGNMENTS

REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS RESULT 1 CNS0091P/c FEATURES COMMENT SOURCE DEFINITION JOURNAL ORGANISM source Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleater de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library fly), g AL05301 Drosophila melanogaster genome sur BACR19D16 of RPCI-98 library from fly), genomic survey sequence. and how to order individual BAC clones, the entire library, filters for hybridization from the BACPAC Resource Center compand at http://bacpac.med.buffalo.edu/drosophila_bac.htm. Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. GSS Genoscope.
Direct Submission Drosophila melanogaster AL053013.1 fruit fly. (bases 1 to 925) /clone_lib="RPCI-98" /organism="Drosophila /db_xref="taxon:7227" Location/Qualifiers GI:4934461 925 bp survey sequence TET3 end of BAC # rom Drosophila melanogaster (fruit melanogaster' Insecta; can part of a

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                                                                                                              Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr )

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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CNS012I3

Drosophila melanogaster genome survey sequence T7 end of BAC
BACN08C07 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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collaboration with the Berkeley Drosophila Genome Project (BBGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RRCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the
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    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as

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- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BBGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BBGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Canadias at the Roswell Park Cancer Institute in Buffalo,
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                                                                                                                                                                                                Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAAASAAASSASSAASVVGAACSSGSGASGSSSAGAARARCASVCASSASSGSCSGCSSS 703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSSSSSAASCSSSSSSSSVAAVCSGSGSGVGVSAAAAVARSGARGMGGMGAAGSGRAV 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCSSCSBSSCSCCASSSRASGCSSSSSSSSSSSSSSSSSGCMCAMSSASSASSSSSAGGSS
                                                                                                                                                                                                                                                                               Pan troglodytes DNA, clone: PTB-089D22.R, genomic survey AG089860
AG089860.1 GI:16641662
GSS; GSS (genome survey serveror)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
                                    2 (bases 1 to 1091)
Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y
                       Direct Submission
                                                                                           Unpublished
                                                                                                                Totoki,Y., Watanabe,H. and Sakak
BAC end sequences of Library PTB
                                                                                                                                                   Fujiyama,A.,
                                                                                                                                                                                          Mammaila;
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                        (sites)
                                                                                                                                                                                                                           troglodytes
                                                                                                                                                                                                                                          : GSS (genome survey sequence).
troglodytes male lymphoblast DNA,
Library clone:PTB-089D22.R.
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/db_xref="taxon:7227"
/dbone_lib="RPCI-98"
/clone="BACR10E16"
/clone="BACR10E16"
/note="end: TET3"
a 67 c 77 g 27 t 383
                                                                                                                                                                                      Eutheria;
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                                                                                                                                               Hattori, M.,
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                                                                                                                                                                                        Primates;
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Pred. No. 0.28;
                                                                                                                                Toyoda, A.,
nd Sakaki, Y.
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                                                                                                                                                                                      Catarrhini;
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                                                        Taylor, T.D.,
                                                                                                                                                   Taylor, T.D., Yada, T.
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                                                          Yada,
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                                                                                                                                                                                                                              ccgcgccgctggctcatgatcggaaccgacccagcaggccgcctactcgaactcgtcgca
                                                                                                                                                                                                                                                                 CCCCACCCCCCCCCAACCCCGCGACGGCGCCAACCCGGCGCCCCAGTCCGCCCAGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193;
                                                 genomic clon
AQ744715
AQ744715.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                      AQ744715

HS_5505_A2_E03_SP6 RPCI-11 Human Male BAC Library Homo genomic clone Plate=1081 Col=6 Row=I, DNA sequence.
 Eukaryota;
           Homo sapiens
                           human
                                                                                                                                                                                        3290
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R.Site 1
R.Site 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="PTB-089D22.R"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Pan troglodytes"
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 Metazoa;
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                                                  GI:5522237
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: SacI.
Chordata;
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Pred. No. 0.
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Craniata;
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 Vertebrata;
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 Euteleostomi;
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GCCCC 156
                                      gcgcc 3234
                                                                                  gcctgacctccacgactcagcacgcaagcactaccaacgagaccggctcgacgacacggc 3169
                                                                                                                                                                                                                                                  gtcgtacccgtgcgtctcgacgcggccaccgttgccgctctcacagaacgagcaacagcc 3049
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                                                                                                                  cgtgctctacgcggccacccacgttctcaactcccggccactcgacgacgaagacgaccc
                                                                                                                                                                  gagggcatcacgaaccgttcagacgcgatccgagccgcagtccacgagtggacacgggtt 3109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
http://www.htsc.washington.edu
plate: 1081 row: I column: 6
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Location/Qualifiers
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High Throughput Sequencin
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Natl. Acad. Sci. U. S. A. 96 (17),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen d and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

183 c 412 g 86 t 50 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="plate=1081 Col=6 Row=I"
/clone_lib="RPCI-11 Human Male I
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
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Pred. No. 1.7;
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Best Local Similarity
Matches 187; Conserv
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ccacgcactgccggaggcagggaacccgcgttcgcaacgtcacccgatcaacggtcggccg 817
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                                                    GACCATCTCACGCGCCATGGTCGGCCGCACCGTCGCCGATGTCGAGCGCGACTTGATCCT
                                                                                                                                        caacgtcaccctgttcgacaccacccgcatgtgggcataccgggccgtccggcactcctg
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                                                                                gggcggcccggtcgccgaatgggagcacaccgtattcgagcacatccacctactgaacga 937
                                                                                                                     CGGCCTCAGCGAGGTCGTCGCCATGGCTTCGGTCGCGACCCAGGCCGCCCAGACCGCCGA
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B96799
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Unpublished (1997)
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1 (bases 1 to 570)
Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K., Golder
RAPTY.K., Granger,D., Suh,E., Wible,C., Adams,M.D. and Venter
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T32L9TR TAMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Eukaryotic Genomics
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Medical Center Dr., Rockville,
301 838 0200
301 838 0208
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1:
; Produced by Rod Wing"
; 232 c 163 g 79 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="T32L9"
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653 gcaccggatcacaaagaacccgctcagcaccgcccatgcgaccctctgggggccccgcaga 712

GGACCGCGACAAGAACCACCTGCGGCTGACCTTCCGCGCCACGCTCATGGGGCCAGGCGTG 132

Matches 154;

Similarity

Conservative

0; Pred.

Mismatches

171;

Indels

0;

Gaps

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RESULT
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further ir
call: (800)-533-4363 or contact via email: ccu@resgen.com
seg primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW132314 448 bp mRNA linear EST 30-NOV-2001 se02e02.yl Gm-c1013 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1013-2355 5' similar to TR:077046 077046 AMINOPEPTIDASE N ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
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                                                                                                                           84
                                                                                                                                                                                                                                          /note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from whole seedlings of 2-3 week old greenhouse grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction
                                                                                                                           Erpelding."
                                                                                                                                                                                                  site of the pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      greenhouse
                                                                                                                                                                        was constructed by Dr. Randy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Whole seedlings,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="GENOME SYSTEMS CLONE ID:
/clone_lib="Gm-c1013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Glycine max"
/db_xref="taxon:3847"
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                       Length 448;
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Beck,C.,
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CCCTGCCCCACGGCGCCCCCCCCCCTCTCCACCCCCACACCCCCCGCACGCTGCGCCCCCC 687
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                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM11175 row: c column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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National Institutes of Health, Mammalian
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5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
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                                                                                                                                                                           /db_xref="taxon:10090"
/clone="IMAGE:5064900"
/clone=NCI_CGAP_Kid14"
/clone_1ib="NCI_CGAP_Kid14"
/lab_host="0H10B (Tl phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. | " a 625 c 311 g 163 t
                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="FVB/N"
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Rodentia;
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Pred. No. 4;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 961)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN03H07 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                        69; Conserv
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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/clone="BACN03H07"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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Drosophila melanogaster genome survey sequence
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Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
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Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
                                                                              Generation of expressed sequence adapted cells of Chlamydomonas re DNA Res. 7 (5), 305-307 (2000)
                                                                                                                                                                         Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                   AV623353 Chlamydomonas
                                                                                                                              Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Nakamura, Y. and Tabata, S.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14B09"
/note="end : T7"
a 202 c 241 g
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Location/Qualifiers
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asamizu@kazusa.or.jp,

URL: http://www.kazusa.or.jp/en/plant/

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RESULT 1
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 645)
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as par
collaboration with the European Drosophila Genome Project (EDM
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
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/clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2"
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/note="Vector: pBluescriptII Sk-; Site_1: EcoR; Site_2: EcoR; Site_
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/strain="C9"
/db_xref="taxon:3055"
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gcaccggatcacaaagaacccgctcagcaccgcccatgcgaccctctggggccccgcaga
                                                                   NTTTSSNNSNSSCNTTSANNTSSTNTTNTAGNNNNATSSSNSNNNSSNNNSNNNSNSSGSG
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/plasmid = "pBeloBAC11"
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/clone= "BACN08C07"
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Search completed: October 6, 2002, 16:22:38 Job time: 17806 sec

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Copyright (c) 1993 - 2000
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Sequence 7, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 6, Appli	Sequence 14, Appl	Sequence 34, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli

ALIGNMENTS

; MOLECULE TYPE: nucleic acid US-07-977-630-1 RESULT 1 US-07-977-630-1/c CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: HELTOD, Charles J. REGISTRATION NUMBER: 28,019 REFERENCE/DOCKET NUMBER: 469 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700 TELEPAX: 201-994-1744 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 6407 nucleotides Sequence 1, Application US/07977630 Patent No. 5583038 GENERAL INFORMATION: SOFTWARE: ASCII CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc APPLICANT: Stover, Charles K. TITLE OF INVENTION: BACTERIAL EXI TITLE OF INVENTION: DA ENCODING NUMBER OF SEQUENCES: 84 CORRESPONDENCE ADDRESS: TYPE: nucleic STRANDEDNESS: TOPOLOGY: cir STATE: New COUNTRY: US ZIP: 07068 COMPUTER: IBM OPERATING SYSTEM: MS-DOS APPLICATION NUMBER: US/07/977,630 FILING DATE: No. 5583038ember 17, 1993 ADDRESSEE: nucleic acid 6 Becker Farm circular Carella, Byrne, Ba Stewart & Olstein double inch diskette 469201-174 Bain, Gilfillan, Cecchi, EXPRESSION VECTORS CONTAINING SECRETION SIGNALS OF LIPOPROTEINS

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Query Match Best Local Similarity Matches 274; Conserv

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DB 1; 2.1e-10; hes 293;

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INFORMATION FOR (
SEQUENCE CHARA)
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                                                            ATTORNEY/AGENT INFORMATION:
NAME: HEITON, Charles J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 465
TELECOMMUNICATION INFORMATION:
                                                                                                                                             SOFFWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,
FILING DATE: NO. 5583038ember
CLASSIFICATION: 435
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MEDIUM TYPE: 3.5 inc
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: MS-DOS
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Stewart & Olstein
                     SEQ ID NO:
                                                                                                                                                                                                                                                               3.5 inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                             BACTERIAL EXPRESSION VECTORS CONTAINING DNA ENCODING SECRETION SIGNALS OF LIPOPROTEINS 84
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RESULT 3
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                                                                                                                                                                                                                     Sequence 20, Application Patent No. 5583038
GENERAL INFORMATION:
APPLICANT: Stover, Ch
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Best Local Similarity
Matches 274; Conserv
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
                                             STREET: 0 LC
CITY: Roseland
CTATE: New Jersey
                                                                                                                                                                                      TITLE OF INVENTION:
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CORRESPONDENCE ADDRESS:
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ilarity 47.8%;
Conservative
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Stewart & Olstein
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Pred. No. 2.1e-10;
                                                                                                                                   Bain,
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RESULT 4
US-07-977-630-21/c
Sequence 21, Application US/07977630
Patent No. 5583038
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Best Local :
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REFERENCE/DOCKET NUMBER: 469
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-94-1700
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ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
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Local Similarity 47.6%;
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SOFTWARE: ASCII
                                                                                                                           GTCAGCAGACCACGTACAAAGCGGCTCCGACGCCCTAGGGGCGAATTGCGCACTGTTCG
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                                                                                                       ATTCCGTCAGGTTGTGGGCCTATCGTCCCGCCC 2954
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Pred. No. 4.4e-10;
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GENERAL INFORMATION:

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REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 469:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 21:
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Best Local Similarity
Matches 273; Conserv
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TITLE OF INVENTION: BACT
TITLE OF INVENTION: DNA
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: nucleic acid
7-977-630-21
                                                                                                                                                                                                                                      1499
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SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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LENGTH: 4120 nucleotid
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ATTORNEY/AGENT INFORMATION:
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TCTACACACTCAGCCACATCGAGGCCGAGCTCGGCGCGAACATGCCACCGCCGCGCTGGC 1260
                                cgctctacgagctgcgcgccctcgcacacaccctcgacgagatccacgcactgccggagg
                                                                           GCCTCATGACCAAAAACCCCGGCCACATCGCCTGGGAAACGGAATGGCTCCACTCAGATC 1320
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Stewart & Olstein
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BACTERIAL EXPI
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Pred. No. 4.4e-10;
0; Mismatches 294;
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Best Local Similarity
Matches 273; Conserv
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TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 11
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REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                  AAAGCCGCGCGTCGGCCCTAGGCCGCCGGTACATCGAGGCGAACCCAACAGCGCTGGCAA 250:
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Pred. No. 4.4e-10;
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PCT-US95-12642-11
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                                                                                                  TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-9043
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/316,950 FILING DATE: 03-OCT-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12642
                                                                                                                                                                                   NAME: HUNTEY, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Mycobacterial Reporter Strains and Uses
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MOLECULE TYPE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                     TYPE: nucleic STRANDEDNESS:
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                        TOPOLOGY:
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RESULT 7
US-08-316-950-15
; Sequence 15, Application US/08316950
; Patent No. 5679515
; GENERAL INFORMATION:
CHARLES K.
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Best Local Similarity
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         TITLE OF INVENTION:
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CITY: S
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LOCATION: 1.4120
OTHER INFORMATION:
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No. 4.4e-10;
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Version #1.
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Best Local Similarity 47.6%;
Matches 273; Conservative
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LENGTH: 4296 base pairs
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REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
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LOCATION:
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                   acaccaccgcatgtgggcataccgggccgtcc 867
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ATTCCGTCAGGTTGTGGGCCTATCGTCCCGCCC
                                                                        GTCAGCAGACCACGTACAAAGCGGCTCCGACGCCGCTAGGGCGGAATTGCGCACTGTTCG
                                                                                                          cagggaacccgcgtcgcaacgtcacccgatcaacggtcggccgcaacgtcaccctgttcg
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Pred. No. 4.5e-10;
0; Mismatches 294;
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PCT-US95-12642-15

Sequence 15, Application PC/TUS9512642

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Best Local
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INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 03-OCT-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                    ccttggtcatcaccgatcgagatgcttcggatgctgactgggccgcagacctcgctgggc 480
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                                                 GGTCCCATCCGCTGCCCAACGCGATCGTGGGCAATCGCGCCAACGGCCACGCACACGCAG
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Pred. No. 4.5e-10;
D; Mismatches 294;
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                                                                                                                                                     ; LOCATION: 1..4352
; OTHER INFORMATION: /standard_name=
US-08-316-950-16
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                                                                    Matches
                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 543-50.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
2405
                                                                                                                                                                                                                        MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 4352 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,4
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: STOVER, Charles APPLICANT: HICKEY, Mark J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2945
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                301 agagctggctgccacgcaagccgctggcgtcagccgagaagtctggggggtaccgggcacg 360
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AGCTCTGGCTGCCGTACTGGCCGCTGGCAAGCGATCTGCTCGAGGGGATCTACCGCC 2464
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                                                                                 Similarity
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                                                                  Conservative
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415) 543-5043
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                                                                Score 80.6; DB 1;
Pred. No. 4.5e-10;
0; Mismatches 294
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PCT-US95-12642-16

Sequence 16, Application PC/TUS9512642

GENERAL INFORMATION:
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                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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APPLICANT: 201 Elliott Avenue West, Suite 150
APPLICANT: Seattle, Washington 98119
TITLE OF INVENTION: Mycobacterial Reporter Strains and
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 18
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                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,950
FILING DATE: 03-OCT-1994
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NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                             FILING DATE: 03-OCT-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                   APPLICATION NUMBER: PCT/
FILING DATE: 02-OCT-1995
CLASSIFICATION:
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INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 4352 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                         Sequence 13, Applicat Patent No. 5679515 GENERAL INFORMATION:
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Best Local Similarity
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                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                          APPLICANT: STOVER, Charles K.
APPLICANT: HICKEY, Mark J.
TITLE OF INVENTION: Mycobacte.
TITLE OF INVENTION: Thereof
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OTHER INFORMATION: /standard_name= "plasmid
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Townsend and Townsend Khourie euart Street Tower, One Market
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Best Local Similarity
Matches 273; Conserv
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TELEFAX: (415) 543-504
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 4505 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
2862 GTCAGCAGACCACGTACAAAGCGGCTCCGACGCCGCTAGGGCCGGAATTGCGCACTGTTCG
                                                                    2802 TCTACACACTCAGCCACATCGAGGCCGAGCTCGGCGCGAACATGCCACCGCCGCGCGCTGGC
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                          775 cagggaacccgcgtcgcaacgtcacccgatcaacggtcggccgcaacgtcaccctgttcg 834
                                                                                                     715 cgctctacgagctgcgcccctcgcacacccctcgacgagatccacgcactgccggagg
                                                                                                                                                                    655 accggatcacaaagaacccgctcagcaccgcccatgcgaccctctggggccccgcagacg 714
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OTHER INFORMATION:
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CLASSIFICATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No. 4.6e-10;
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Best Local Similarity
Matches 273; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4505 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                    2502 ACCTGCTGGTCGTGGACGTAGACCATCCAGACGCAGCGCTCCGAGCGCTCAGCGCCCGGG 2561
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                                                                                                                                                                                    2382 AGCTCTGGCTGCCGTACTGGCCGCTGGCAAGCGACGATCTGCTCGAGGGGATCTACCGCC 2441
                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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481
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OTHER INFORMATION:
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VENTION: Mycobacterial Reporter Strains and
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euart Street Tower, One Market Plaza
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Pred. No. 4.6e-10;
0; Mismatches 294;
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US-08-316-950-12
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                                                                                                                                             REFERENCE_DOCKET NUMBER: 1537
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 6047 base pairs
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                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08,
FILING DATE: 03-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
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MEDIUM TYPE: Floppy disk
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                                                                                  MOLECULE TYPE:
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            NAME/KEY: misc_fea
LOCATION: 1..6047
OTHER INFORMATION:
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                                                                                                  TOPOLOGY: 11
                                                                                                                                                                                                                                                                     NAME: Hunter, Tom REGISTRATION NUMBER:
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Steuart Street Tower, One Market Plaza
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RESULT 14
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Best Local Similarity 47.6%;
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PathoGenesis Corporation APPLICANT: 201 Elliott Avenue West, APPLICANT: Seattle, Washington 98119
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CLASSIFICATION:
                                     APPLICATION NUMBER:
                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                  STREET: Steuart Street Tower, One CITY: San Francisco
                                                                                                                                                                                                                                                                             ADDRESSEE:
                    FILING DATE:
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Pred. No. 5e-10;
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Best Local Similarity
Matches 273; Conserv
Sequence 17, Application US/08316950 Patent No. 5679515
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TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 12:
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LENGTH: 6047 base pairs
TYPE: nucleic acid
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                                                                                                         2945 ATTCCGTCAGGTTGTGGGCCTATCGTCCCGCCC 2977
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REGISTRATION NUMBER: 38,498
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LOCATION: 1..6047
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Pred. No. 5e-10;
0; Mismatches 2
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INFORMATION FOR SED ID NO: 17
SEQUENCE CHARGITERISTICS:
LENGTH: 6171 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                         2682 ACATGGCGGCGTGCGCCGAAGGCCTTCGGCGCGCCGTCGATGGCGACCGCAGTTACTCAG 2741
                                                                                                                     2622 TGTGGGCACTCAACGCCCCTGTTCCACGCACCGAATACGCGCGGGGGTAAGCCGGTCGCAT 2681
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FILING DATE: 03-OCT-
CLASSIFICATION: 435
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OPERATING SYSTEM:
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OTHER INFORMATION: /standard_name=
OTHER INFORMATION: pMV261-lux*
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TOPOLOGY: 11r
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accggatcacaaagaacccgctcagcaccgcccatgcgaccctctggggccccgcagacg 714
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Similarity 47.6%;
73; Conservative
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SYSTEM: PC-DOS/MS-DOS
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Maximum Match 100%
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1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*

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Copyright (c) 1993 - 2000 Compugen
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AAW14835
AAR20992
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Protein encoded by
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Drosophila melanog
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ALIGNMENTS

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AAY44636 standard; Protein; 303 AA

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ANY44636
ID ANY44636
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AC ANY4
A Propionibacterium LMG 16545; vector; plasmid; antigen; vaccine; enutritional factor; growth factor; clotting factor; antimicrobial hormone; vitamin B12; animal feed; lactic acid bacteria; foodstuf 07-APR-2000 Propionibacterium LMG 16545 protein-1. AAY44636; bacteria; foodstuff; 252

drug;

Propionibacterium freudenreichii LMG 16545

WO9967356-A2

29-DEC-1999.

25-JUN-1999; 99WO-EP04416

25-JUN-1998; 98EP-0305033

(KONN) GIST-BROCADES BV.

Pouwels PH, Van Luijk N, Jore JPM, Luiten

WPI; 2000-136977/12. N-PSDB; AAZ49691.

Novel vectors containing Propionibacterium sequences, used to homologous or heterologous proteins $\,$ express

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AAW14835
ID AAW1
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AC AAW1
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Best Local
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17-NOV-1992;
21-OCT-1991;
                                                                                                                                                                                    Plasmid pMV101; Mycobacteria; lipoprotein secretion signal sequence; antigen; bacterial vaccine; Lyme disease; Borrelia burgdorferi;
                                                                                                                                                                                                                                                                                                                               AAW14835 standard; Protein;
                                             21-OCT-1991;
                                                                                                                                                                                                                                    Protein
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 92US-0977630.
91US-0780261.
                                             91US-0780261
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                                                                                                                                                                                                                                   M.rep ORF2 of plasmid pMV101.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacteria expressing secretion signal of lipoprotein and heterologous antigen, esp. outer surface protein A or B of Borrelia burgdorferi - are used in the form of a live bacterial vaccines
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N-PSDB; AAT64413.
                                                                              03-JUN-1992
                                                                                                                                                    AAR20992 standard; Protein;
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Pred. No. 6.8e-26;
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10;

Polymerase chain resistance; BCG;

reaction; mycobacterial promoter; kanamycın; Bacille Calmette-Guerin; origin of replication.

Protein "e" encoded by mycobacterial plasmid pMV101.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                덩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmid pYUB12 was constructed by ligating a 5kb Sau3 fragment from CD pAL5000 (contg. a replication origin from M.fortuitum) to BamHI-CD dispested pIJ666 (contg. an E.coli ori and kanamycin-neomycin resistance sequences). A 2566bp HpaI-EcoRV fragment from pYUB12 (comprising the minimum sequence necessary for plasmid replication in BCG) was ligated to PvuII-digested pYUB8 to form pYUB53. (Plasmid CD pYUB8 is a pBR322 deriv, which includes an E.coli replicon and a kanamycin resistance gene). Twelve restriction sites were removed by digesting pYUB53 with Aatl, EcoRV and PstI. To eliminate 792 chases of the (inactivated) tet gene, the plasmid was digested with CO warI and the 6407bp gel purified fragment was religated/CD the nucleotide sequence of plasmid pWI01 is printed in the specification but the copy quality is too poor to allow the specification but the copy quality is too poor to allow the squence to be included on the GENESEQ nucleotide database.

Three proteins are encoded by pWV101, i.e. the kanamycin resistance protein and proteins "d" and "e" encoded by the complementary contents also AAR20991 and AAR20993.
                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA site-specific integration into Mycobacteria - useful as adjuvant in vaccines and as therapeutic agent for malaria, influenza, herpes and human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 24; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9201783-A
 347
                                                                                                                                                                                        181
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                               280
                                                            294
                                                                                          229
                                                                                                                         234
                                                                                                                                                         173
                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                    66
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                N
                                                                                                                                                                                                                                                                                                             defeq1----wlpywplasddllegiyrg-srasalgrryieanptalanilvvdvdhpd
                                                                                                                                                                                                                                                                                                                                                DSFETLFPESWLPRKPLASAE-KSGAYRHVTRQRALELPYIEANPLVMQSLVITDRDASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1992-064943/08
                                                                               FATGPLGLNELKHLSRSISRW-----VWRN---FTPETFRARQKAISLRGASKGGKEGG
                                                                                                                                                                                   avdgdrsysglmtkwpgeiawetewlhsd----lytlshieaelganmpp---prwrqqt 233
                                                                                                                                                                                                               VLGGDASYGHRITKNPLSTAHATLWGPADALYELRALAHTLDEIHA-LPEAGNPR-----
                                                                                                                                                                                                                                                aalralsargshplpnaivgnranghahavwalnapvprteyarrkplaymaacaeglrr
                                                                                                                                                                                                                                                                    ADWAADLA--GLPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCD 118
                               HKGGIASGASRRA
                                                           vcpgplpdsevraiansiwrwittksriwadgivvyeatlsarqsaisrkgaa-----
                                                                                                                        tynaaptplgrncalfdsvrlwayrpalmriylptrnvdglgraiyaecrarnaefpcnd
                                                                                                                                                     -RNVTRSTVGRNVTLFDTTRMWAYRAVRHSWGGPVAEWE---HTVFEHIHLLNETIIADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNIV OF PITTSBURGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hatfull G;
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90US-0553907
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                             292
 358
                                                                                                                                                                                                                                                                                                                                                                                              19.7%;
                                                                                                                                                                                                                                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                                             Score 315; DB 1
Pred. No. 2e-24;
9; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                   DB 13;
                                                                                                                                                                                                                                                                                                                                                                                 128;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 368;
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                   180
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                                                                                                                                                                                                                                                                                                                                              60
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AAR34543
ID AAR3
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                                                                                                                                                                                                                   This sequence is the tet d gene product encoded by plasmid pMV101. When the nucleotide was decoded, the sequence in the specification was found to contain several deletions and insertions which upset the reading frame. Also many codons were found to encode amino acids contrary to the universal genetic code. In addition two amino acids in the sequence in the specification were given as X and were further defined.
                                                                                                                                                                                                                                                                                                                                                                       Expression vector for expressing protein or polypeptide in mycobacterium - conty DNA sequences encoding lipoprotein secretion signal and peptide heterologous to bacteria expressing fusion protein of lipoprotein heterologous to bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytotoxic T-lymphocyte response; transformed Mycobacteria; Mycobacterium smegmatis; vaccine; cell mediated immunity; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR34543 standard; Protein;
                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tet d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR34543;
                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MEDI-) MEDIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-OCT-1992;
                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 5; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-APR-1993.
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  181
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1993-152187/18.
DB; AAQ41316.
                   VLGGDASYGHRITKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEAGNP----RRN
                                                                                                 defeq1---wlpywplasddllegiyrq-srasalgrryieamptalanllvvdvdnpd
v-dgdrsysglmtkmpghiawetew-----lhedlytlseieaelgawmppprwrqq
                                                 aalralsargsnp
                                                                                                                          DSFETLFPESWLPRKPLASAE-KSGAYRHVTRQRALELPYIEANPLVMQSLVITDRDASD
                                                                         ADWAADLA--GLPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product
                                                                                                                                                                                                                   367 AA;
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92WO-US09075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                 lpnaivgnrangnaeavwalnapvprteyarrkplatmaacaeglrr 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    influenza virus; CTL; herpes
                                                                                                                                                               18.0%; Score 287.5; DB 14; 33.3%; Pred. No. 1.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "X undefined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pMV101 - a deletion mutant of pYUB125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           undefined
                                                                                                                                                   35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367
                                                                                                                                                      Mismatches 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification'
                                                                                                                                                      Indels
                                                                                                                                                                             Length
                                                                                                                                                                              367;
                                                                                                                                                   37;
                                                                                                                                                  Gaps
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231
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RESULT
AAR29622
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                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                    Method of inducing cytotoxic T-lymphocyte response - esp. expression products of transformed Mycobacterium are useful as vaccines against HIV, pertussis, malaria, influenza virus, herpes
                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                  This sequence is the tet d gene encoded by plasmid pMV101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytotoxic T-lymphocyte response; transformed Mycobacteria; Mycobacterium smegmatis; vaccine; cell mediated immunity; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tet d gene product from pMV101 - a deletion mutant of pYUB125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR29622 standard; Protein;
                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 5; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ31727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-433380/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dela Cruz V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MEDI-) MEDIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09221376-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pertussis; malaria;
    185
                             240
                                                       125
                                                                                  183
                                                                                                                                        131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 dvcpgplpdsevralawsiwrwittxsriwadgivvyeatlsarqsaisrkgaa
                                                                                                             73
                                                                                                                                                                13
                                                                                                                                                                            71 PSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYGHRI 130
                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ഗ
raiawsiwrwittxsriwadgivvyeatlsarqsaisrkgaa 226
                         KHLSRSISRW-----VWRN---FTPETFRARQKAISLRGAS
                                                    ncalfdsvrlwayrpalmriylptrxvdglgraiyaecrarnaefpcndvcpgplpdsev 184
                                                                                                       tkmpghlawetew-----lhedlytlseleaelgawmppprwrqqttykaaptplgr 124
                                                                                                                                     TKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEAGNP----RRNVT----RSTVGR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttykaaptplgrncalfdsvrlwayrpalmriylptrxvdglgraiyaecrarnaefpcn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VT----RSTVGRNVTLEDTTRMWAYRAVRHSWGGPVAEWE---HTVFEHIHLLNETIIAD 227
                                                                               NVTLFDTTRMWAYRAVRHSWGGPVAEWE----HTVFEHIHLLNETIIADEFATGPLGLNEL 239
                                                                                                                                                               plpnaivgnrangnaeavwalnapvprteyarrkplatmaacaeglrravdgdrsysglm 72
                                                                                                                                                                                                                                                                                         248
                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stover CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91US-0711643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92WO-US04538
                                                                                                                                                                                                                  13.7%; Score 218; DB 13; 30.6%; Pred. No. 1.9e-14; ative 30; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             influenza virus; CTL; herpes virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                           272
                                                                                                                                                                                                                                               Length 248;
                                                                                                                                                                                                                     Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272
                                                                                                                                                                                                                    Gaps
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AAB35246
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                                                                                                               RESULT
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Best Local S
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              Tetanus vaccination - by transformed Mycobacteria
                                                 08-MAY-2001
                                                                       AAB35246;
                                                                                          AAB35246 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                     This sequence is the tet d gene encoded by plasmid pMV101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-433378/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytotoxic T-lymphocyte response; transformed Mycobacteria; BCG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tet d gene product from pMV101 - a deletion mutant of pYUB125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR37872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR37872 standard; Protein;
                            Corynebacterium thermoaminogenes plasmid pYM4 rep protein
                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 5; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dela Cruz V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9221374-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pertussis; malaria; influenza virus; CTL; herpes virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MEDI-) MEDIMMUNE INC.
                                                                                                                                                                                  125 ncalfdsvrlwayrpalmriylptrxvdglgraiyaecrarnaefpcndvcpgplpdsev 184
                                                                                                                                                                                                                                         131 TKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEAGNP----RRNVT----RSTVGR 182
                                                                                                                                                                                                        183 NVTLFDTTRMWAYRAVRHSWGGPVAEWE---HTVFEHIHLLNETIIADEFATGPLGLNEL 239
                                                                                                                                            185 raiawsiwrwittxsriwadgivvyeatlsarqsaisrkgaa
                                                                                                                                                                240 KHLSRSISRW-----VWRN---FTPETFRARQKAISLRGAS
                                                                                                                                                                                                                                                                    73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                           tkmpghiawetew-----lhedlytlseieaelgawmppprwrqqttykaaptplgr 124
                                                                                                                                                                                                                                                                                                               68;
                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                              Conservative
                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stover CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-0711084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92WO-US05023
                                                                                                                                                                                                                                                                                                                        13.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      provoking an immune response using
                                                                                                                                                                                                                                                                                                              30;
                                                                                          458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248
                                                                                                                                                                                                                                                                                                             Score 218; DB 13;
Pred. No. 1.9e-14;
0; Mismatches 96;
                                                                                          ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mediated
                                                                                                                                             226
                                                                                                                                                                272
                                                                                                                                                                                                                                                                                                                                  Length 248;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                             28;
                                                                                                                                                                                                                                                                                                             Gaps
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6,

high temperature

Plasmid; pYM4; rep; coryneform bacterium; L-amino acid; thermostable;

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RESULT AAB35243 ID AAB35243 AC AAB5 XX AB5 XX COT)
DE COT)
XX Plai KW Plai KW high XX AC ACT)
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Best Local S
Matches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides plasmids isolated from Corynebacterium thermoaminogenes encoding a rep protein. These are useful for improving Coryneform bacteria, which are capable of growing at elevated temperatures and of producing substances such as L-amino acids. The present sequence is the rep protein from a Coryneform bacterial plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matsuzaki Y,
Sugimoto S;
                      Plasmid; pYM1; rep; coryneform high temperature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium
                                                        Corynebacterium
                                                                               08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New plasmids derived from Corynebacterium thermoaminogenes, useful improving coryneform bacteria, which can grow at elevated temperatuand for producing useful substances (e.g. L-amino acids)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AJIN ) AJINOMOTO CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-AUG-1999;
 Corynebacterium
                                                                                                      AAB35243;
                                                                                                                           AAB35243 standard; Protein; 492
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                                                                                                                                                                                                                                                                                                                                                                                         SPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYGHRIT 131
                                                                                                                                                                                  --qptvsarstqtqssrgrkalatmgrrgaatsnarrwadpesdyarqtrerlarams
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                                                                                                                                                                                                                            agerlkdtk1idayeraynvaqavgadgrepdlpamrdrqtlarrvrayvakg-----
                                                                                                                                                                                                                                                   --HLLNETIIADEF-----ATGPLG-----LNELKHLSRSISRWVWRNFTPETFR 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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 thermoaminogenes
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Pred. No. 0.026; 
2; Mismatches 1
                                   bacterium;
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                                                      pYM1 rep protein.
                                  L-amino acid; thermostable;
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 WO200171042-A2
                                                       Drosophila;
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                                                                                                                          ABB69873;
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The present invention provides plasmids isolated from Corynebacterium thermoaminogenes encoding a rep protein. These are useful for improving Coryneform bacteria, which are capable of growing at elevated temperatures and of producing substances such as L-amino acids. The present sequence is the rep protein from a Coryneform bacterial plasmid.
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Drosophila melanogaster.
                                                                               Drosophila melanogaster polypeptide SEQ
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N-PSDB; AAF24439.
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                                                                                                                                                                                                                                                              368 --qptvsarstqtqssrgrkalatmgrrggqk
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55; Conserv
                                              developmental
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                                                biology;
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42; Mismatches
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                                              signalling;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
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                                                              Plasmid;
                                                                                      Corynebacterium thermoaminogenes plasmid pYM3 rep protein.
                                                                                                                 08-MAY-2001
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New plasmids derived from Corynebacterium thermoaminogenes, improving coryneform bacteria, which can grow at elevated to and for producing useful substances (e.g. L-amino acids) -
                                                                              Plasmid;
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                                                                                                                             08-MAY-2001
                                                                                                                                                     AAB35244;
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Sugimoto S;
                                            Corynebacterium
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                                           thermoaminogenes
                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.0%;
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                                                                            coryneform
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                                                                              bacterium;
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No. 0.33;
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                                                                              L-amino
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d temperatures,
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RESULT 12
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AC AAG9077
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DT 26-SEP
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Matches 58
                                                                                                                                                                                                                                                                          C glutamicum protein
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     18-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New plasmids derived from Corynebacterium thermoaminogenes, useful for improving coryneform bacteria, which can grow at elevated temperatures, and for producing useful substances (e.g. L-amino acids) -
                                                    20-JUN-2001
                                                                                                                                                     Corynebacterium
                                                                                                                                                                                                                           Coryneform bacterium; amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRARQKAISLRG----ASKG-----GKEGGHK 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kaagerlkdakiidayeraynvaqavgadgrepdlpamrdrqtmarrvrayvakg-----
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                                                                                                                                                                                                      acid synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qptvsarstqtqssrgrkalatmgrrggqk
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     2000EP-0127688
                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                     glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                             fragment SEQ ID NO:
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21.2%; Pred. No. 0.
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                                                                                                                                                                                                                              acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                  610
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Query Match
Best Local Similarity
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07-APR-2000;
03-AUG-2000;
                                                                                                                   mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                            The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. I are useful for identifying the mutation point of a gene derived from
                                                                         Sequence
                                                                                                          European Patent Office.
                                                                                                                                                                                                                                                                                                                         Claim 17; SEQ ID NO: 4495; 246pp + Sequence Listing; English
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   68;
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; 2000JP-0280988.
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Senoh A, Ik
            5.68;
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ID AAE1
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29-NOV-2001
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                                                                                                                                                                                                                                                        ADEFATGPLGLNELKHLSRSISRWVWRNFTPE-----
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(first entry)
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                                                                   Protein;
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10-APR-2000;
14-APR-2000;
                                                                                                                                                                                                                                                                                                                       The present invention relates to the cloning and sequencing of the cluster encoding a modular type I polyketide synthase (PKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antifungal antibiotics. The present sequence is a transcriptional activator encoding Streptomyces nours nystatin gene, ORF2.
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(SNTF )
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(SINV-)
(DZIE/)
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                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 179; 266pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               New nystatin polyketide synthase polynucleotides useful as antibiotics and antifungals -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces
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                         246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (STRO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FJAE/)
   280
                                                 228
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                                                                                                                       128
                                                                                                                                              152
                                                                                                                                                                   74
                                                                                                                                                                                                                  16
                                                                                                                                                                                           93
                                                                                                                                                                                                                 KPLASAEKSGAYRHVTRQRALELPYIEANPLVMQSLVITDRDASDADWAA--DLAGLPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-557614/62.
DB; AAD17184.
isrhnlhlvawvrslddagrfevrlaeraadltvteravalwhmkhgghlldeegyrvgv
                           ISR----
                                               aadmlha---
                                                                                                                                                                  SYVSMNRVTTTG-HIVYALKNPVCLTDAARRR----PINLLARVEQGLCDVLG--GDASYG 127
                                                                                                                                                                                         ralaaaphvvalshvtgdrdlqlnvmardpamlsrwvthdlaaldgvraarthlag-pvh 151
                                                                    DTTRMWAYRAVRHSWGGPVAEWEHTVFEHIHLLNETIIA--DEFATGPLGLNELKHLSRS
                                                                                                                   HRITKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEAGNPRRNVTRSTVGRNVTLF
                                                                                                                                           tegsrwrlralgrhqvarl----aadasrhrtdtpafvldeldgqlvtalsvdgraty-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     တ
                                                                                                                                                                                                                                         1 Similarity
79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2OTCHEV S B.
SEKUROVA O N.
FJAERVIK E.
BRAUTASET T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SB, Sekurova O
, Ellingsen TE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SINVENT AS.
DZIEGLEWSKA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNIV NORGES TEKNISK NATURVITENSKAPELIGE SINTEF STIFTELSEN IND TEK FORSK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STROM
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                                                                                                                                                                                                                                                                                                  354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000GB-0002840.
2000GB-0008786.
2000GB-0009387.
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                         WWRNFTPETFRAR----
                                              rcevarplsewpyty----siwgqvpaarlrevtrrytgmrevrlcasy
                                                                                                                                                                                                                                                   25.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sletta
                                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fjaervik E, Brautaset
letta H, Gulliksen O;
                                                                                                                                                                                                                                                  Score 89; DB Pred. No. 1.3;
                                                                                             -rala---eqcgagpd--tvrrrvqr-----lf
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                                                                                                                                                                                                                                         Mismatches 114;
                        -QKAISLRGASKGG---KEGGHKGGI
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                        284
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RESULT 1
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                                                                                                                                                   Query Match
Best Local
                                                                                                                                       Matches
                                                                                                                                                                                                                                                              capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                               (ABB57737-ABB72072)
The sequence data f
specification, but
                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200171042-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster polypeptide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB70548 standard; Protein; 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB70548;
 494
                       103
                                              434
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                                                                   45
                                                                                                                                                Local
                                                                                                               4 FETLFPESWLPRKPLASAEKSGAYRHVTRQRALELPYIE----
                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                   invention relates to an
vvpvprptfapeppldvvettasthhlwtevpttaapffteypaevlitthrtsagrftt
                      RRPINLLARVEQGLCDVLGGDASYGHRITKNPLSTAHATLWGPADALYE-----
                                           psitisvditssgssssssssesvevfttpapvfvqrvttietsisidyvtptplpetttpr 493
                                                                  PLVMQSLVITDR-DASDADWAADLAGLPSPSYVS-MNRVTTTGHIVYALKNPVCLTDAAR 102
                                                                                       fttlpp---lpgkpqtsassessgevvtseeyttvphfevsgsksesgseevttvrptaa 433
                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASGASRRAHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             JC,
                                                                                                                                       64;
                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             ABL14651.
                                                                                                                                                                                               838
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                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developmental
                                                                                                                                       Conservative
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2000US-0614150
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                                                                                                                                                                                                                                       for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ×
                                                                                                                                               5.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                       38436; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ľ
                                                                                                                                                                                                                               obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PWD,
                                                                                                                                                                                                                                                                                                                                                                                         detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biology;
                                                                                                                                       29;
                                                                                                                                      Score 89; DB 1
Pred. No. 4.5;
29; Mismatches
                                                                                                                                                                                                                                                                                                                                 isolated nucleic acid detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO
                                                                                                                                                            22;
                                                                                                                                      118;
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                                                                                                                                                                                                                               format
                                                                                                                                                                                                                                        part of the
                                                                                                                                                           Length 838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               insecticide;
                                                                                                                                                                                                                              of the printed directly from
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                                                                                                                                                                                                                                                                                                                                 reagent
                                                                                                                                                                                                                                                                                                                                                                                         0 or more cell-
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                      151
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밁 Q 망 Ş

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RESULT 15
ABG29396
The invention relates to isolated polynucleotide (I) and collective (II) sequences. (I) is useful as hybridisation probes, complymerase chain reaction (PCR) primers, oligomers, and for chromosome and in recombinant production of (II). The collective are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating the polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications in cut diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and camino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed septification, but was obtained in electronic format directly from WIPO at the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodyversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID No 59755; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-639362/73.
N-PSDB; AAS93583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG29396 standard; Protein; 905
                                 at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #29387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       АВG29396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hhhphheaegttlqpleedeh--hhhhh-----hdeftt 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YRAVRHSWGG----PVAEWEHTVFEHIHLLNETIIADEFAT 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0540217.
2000US-0649167.
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Sequence

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  376
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                                                                                                                                                                    226 qpsdscqeysdwkekkt-----ylnpwkkidsa--
                                                                                                                                                                                               70 LPSPS---YVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASY 126
                                                                                                                                                                                                                                                    27 YRHVTRQRALE-----LPYI-----EANPLYMQS--LVITDRDASDADWAADLAG 69
                                                                                                           dhqtsvqqlpgeffslenpsdaealyetssglntlse-hgssehgsskhtvaehtsge--
qpsdeqpsgehgsge 390
                           --ADEFATGPLGLNE 238
                                                                                                                                       GHRITKNPLSTAHATLWGPAD--ALYELRALAHTLDEIHALPEAGNPRRNVTRSTVGRNV 184
                                                                                  TLFDTTRMWAYRAVRHSWGGPV----AEWEHTVFEH-----IHLLNETII-----
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                  Conservative
                                                     -haesehasgepaatehaegehtvgeqpsgeqpsgehlsgeqplselesge 375
                                                                                                                                                                                                                                                                                              5.5%;
                                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                                                                                              Score 88;
Pred. No.
                                                                                                                                                                                                                                                                              Pred. No. 6.4;
7; Mismatches
                                                                                                                                                                                                                                                                                              6.4;
                                                                                                                                                                                                                                                                                                            DВ
                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                  -plgtssqpne----lsg--si 268
                                                                                                                                                                                                                                                                                  87;
                                                                                                                                                                                                                                                                                                           Length 905;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                  78;
                                                                                                                                                                                                                                                                               Gaps
                                                                                  225
                                                                                                             325
                                                                                                                                                                                                                                                                                 15;
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Search completed: October 4, 2002, 15:34:40 Job time: 93 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

OM protein protein search, using sw model

4 2002, 15:33:08; Search time 28.21 Seconds (without alignments) 1032.083 Million cell upd

cell updates/sec

Title: Perfect score: US-09-720-583A-2 1596

1 MDSFETLFPESWLPRKPLAS....IASGASRRAHTRQQFLEGLS 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum Maximum BB BB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

score g No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	1	No.	Result
84	84.5	84.5	84.5	84.5	85	85	85	85	85.5	85.5	86	86	86.5	87	87	87.5		89	89	89.5	93.5	97.5	98	100	198.5	282.5	282.5	329	Score	
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989	4302	500	355	355	900	409	356	356	1366	1217	672	672	497	487	457	409	303	4558	1216	606	228	1876	1461	99	248	304	297	336	Length	
Ν.	2	N	N	N	N	N	N	N	N	N	N	2	Ν	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	B	
C90948	A38971	T36090	AE3008	н98275	JH0157	T06767	AE2978	H98304	T35985	T00270	T03457	JC4637	T14609	S60675	S03321	T14611	T36509	C82199	T09224	T37217 ·	н72703	E97944	870588	S32700	S32701	S04456	S0445 5	JS0052	ID	
proteinase II (imp	polycystic kidney	probable integral	monooxygenase [imp	mtaG protein (AF18	cellulase (EC 3.2.	probable transcrip	alkanesulfonate mo	fmnh2-dependent al	probable large Pro	O		transketolase (EC	alanine transamina	hypothetical prote	regulatory protein	alanine transamina	probable molybdopt	RTX toxin RtxA VC1	spindle assembly c		probable translati	zinc metalloprotei	~	hypothetical prote			ř	·ΜΥ	Description	

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30
82	82.5	82.5	82.5	83	83	83	83	83	83.5	83.5	83.5	83.5	83.5	84	84
5.1	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.2	5.3	5.ω
497	1116	1116	814	686	639	559	285	251	1822	1815	863	450	450	1693	686
Ν	N	N	Н	Н	N	N	N	N	N	N	_	N	N	N	2
T47715	AC2921	D97695	GNMSIP	E64946	D82809	G83024	177964	157999	F87203	S73021	GNHYIH	E98122	E95257	AC3240	G85796
hypothetical prote	cobalamin biosynth	cobN protein homol	retrovirus-related	oligopeptidase B (exodeoxyribonuclea	probable acetolact	SP-10 - western ba	SP-10 - western ba	polyketide synthas	polyketide synthas	retrovirus-related	replicative DNA he	replicative DNA he	helicase, SNF2 fam	proteinase II [imp

ALIGNMENTS

37K protein - Mycobacterium fortuitum plasmid pAL5000 C;Species: Mycobacterium fortuitum C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 10-Dec-1999

C; Accession: JS0052;

R;Rauzier, J; Moniz-Pereira, J; Gicquel-Sanzey, B. Gene 71, 315-321, 1988
A;Title: Complete nucleotide sequence of pAL5000, a plasmid A;Reference number: JS0052; MUID:89138007
A;Accession: JS0052

from

Mycobacterium fortui

A; Molecule type: DNA A; Residues: 1-336 < RAU>

as

for e 18 residue as Trp

A; Note: the authors translated the initiation codon GTG for A; Note: the authors translated the codon ACA for residue: R; Labidi, A.; Mardis, E.; Roe, B.A.; Wallace Jr., R.J. Plasmid 27, 130-140, 1992

A; Title: Cloning and DNA sequence of the Mycobacterium for A; Reference number: JQ1440; MUID:92311251

A; Accession: JQ1440

A; Molecule type: DNA
A; Residues: 160-336 < LAB> fortuitum var fortuitum plasmi

A;Cross-references: GB:M60875; NID:g149984; PIDN:AAA25372.1; PID:g149985 A;Experimental source: var. fortuitum C;Genetics:

A; Genome: plasmid

C; Function: A; Start codon: GTG

A; Description: this protein is involved in the initiation of plasmid replication C; Superfamily: Mycobacterium hypothetical 37K protein

δÃ 맑 Ş 밁 Š 뫄 Ş Matches 104; Query Match Best Local : 177 --RSTYGRNYTLFDTTRMWAYRAVRHSWGGPVAEWE---HTVFEHIHLLNETIIADEFAT 231
: :|| | || :: :: | | :: 149 119 VLGGDASYGHRITKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEAGNPRRNVT-- 176 Watch 20.6%; Local Similarity 33.5%; 89 61 ADWAADLA--GLPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCD 118 34 DEFEQL----WLPYWPLASDDLLEGIYRQ-SRASALGRRYIEANPTALANLLVVDVDHPD 2 DSFETLFPESWLPRKPLASAE-KSGAYRHVTRQRALELPYIEANPLVMQSLVITDRDASD AALRALSARGSHPLPNAIVGNRANGHAHAVWALNAPVPRTEYARRKPLAYMAACAEGLRR 148 Conservative 39; Score 329; DB 2; L Pred. No. 5e-20; 9; Mismatches 131; -LYTLSHIEAELGANMPPPRWRQQTTYK 204 Length 336; Indels 36; Gaps 88 60 10;

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205 AAPTPLGRNCALEDSVRLWAYRPALMRIYLPTRNVDGLGRAIYAECHARNAEFPCNDVCP 264

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hypothetical protein - Escherichia coli plasmid ColE2
C;Species: Escherichia coli
C;Date: 04-Dec-1992 *sequence_revision 04-Dec-1992 *text.
C;Accession: S04455
R;Yasueda, H.; Horii, T.; Itch, T.
Mol. Gen. Genet. 215, 209-216, 1989
A;Title: Structural and functional organization of ColE2
A;Reference number: S04455; MUID:89218922
A;Accession: S04455
A;Status: not compared with conceptual translation
A;Residues: 1-297 <YAS>
C;Genetics:
A;Genome: plasmid
C;Superfamily: Mycobacterium hypothetical 37K protein
                                                                                                              RESULT 3
S04456
hypothetical protein - Escherichia coli plasmid ColE3
C;Species: Escherichia coli
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change;
C;Accession: S04456
R;Yasueda, H.; Horii, T.; Itoh, T.
Moi. Gen. Genet. 215, 209-216, 1989
A;Title: Structural and functional organization of ColE2 and Coli
A;Reference number: S04455; MUID:89218922
A;Accession: S04456
A;Status: not compared with conceptual translation
                                        A; Molecule type: DNA
A; Residues: 1-304 < YAS>
A; Cross-references: GB: D30055;
C; Genetics:
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Best Loc
Matches
Superfamily: Mycobacterium hypothetical 37K protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TKNPLSTAHATLWGPADALYELRALAHTLDEI-HALPEAGNPRRNVTRS-TVGRNVTLFD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAPNITVKNPRNGHAHLLYALALPVRTAPDASASALRYAAAIERALCEKLGADVNYSGLI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPRKPLASAEKSGAYRHVTRQRALELPYIEAN-PLVMQSLVI-TDRDASDADWAADLAGL 70
                          plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                RWVWRNFTPETFRARQKAISLRGASKGGKEG-----GHKGGIASGASRRAHTRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CKNP---CH----PEWQEVEWREEPYTLDELADYLDLSASARRSVDKNYGLGRNYHLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYGHRI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPHKPYCTNDFAYGVRILPKNIAILARFIQQNQPHALYWLPFDVDRTGASIDWSD--RNC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPLGLNELKHLSRSISRW-----VWRN---FTPETFRARQKAISLRGASKGGKEGGHKG
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                                                            NID: 9487267; PIDN: BAA06293.1;
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R;Shi, SL; Wang, Z.X.; Deng, I.; "...", ....
submitted to the EMBL Data Library, March 1993
submitted to the EMBL Data Library, March 1993
A;Description: Complete nucleotide sequence of a plasmid pXZ10142 from Corynebacteriu
A:Reference number: S32699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein 3 - Corynebacterium glutamicum
C;Species: Corynebacterium glutamicum
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
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S32701
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A; Residues: 1-248 <S
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R; Shi, S.L.; Wang,
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Best Local :
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                                  276
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228
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                                                                                                                                                                                                                                                                                                               73 PSYVSMNRVTTT-----
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                                KEGGHKGG
                                                                   QELFSE-----PLPVAEVDQIARSIHRWIITKSRMWTD-GPAVYEATFTTIQ---ATRGK 227
                                                                                       ETIIADEFATGPLGLNELKHLSRSISRWV------WRNFTPETFRARQKAISLRGASKGG 275
                                                                                                                                    GFMPPESWKKTRKSPIGLGRNCALFESARSWAYREIRHHFGDPDG-LGRSIQATAQALN 176
                                                                                                                                                                                                         AQALAYAAAVTEGLRRSVDGDKGYSGLITKNPEHTAWDSHW-VTDKLYTLDELRFWLEET 117
                                                                                                                                                                                                                                                                              PSRISWSSTSTSRTHSCVRCGTETAGGLTPWLKTPF---KRARTRRVGARGAIYPHRVRQ
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RSAEHRWG
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                                                                                                                                                                                                                                            -----LLARVEQGLCDVLGGDASYGHRITKNPLSTAHATLWGPADALYELRALAHTLDEI 162
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68; Conser
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235
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27.48;
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5:
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Pred. No. 3.5e-16;
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hypothetical protein 2 - Corynebacterium glutamicum C;Species: Corynebacterium glutamicum C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 c;Accession: S32700; S32199

20-Feb-1995 #text_change 03-Aug-1995

S32700

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C;Superfamily: Mycobacterium tuberculosis mbtE protein; acetate--CoA ligase C;Keywords: carrier protein; phosphopantetheine; phosphoprotein F;517-949/Domain: acetate--CoA ligase homology <ACL>F;964-1031/Domain: acyl carrier protein homology <ACP>F;996/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable polyketide synthetase mbtf [similarity] - Mycobacterium tuberculos
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 03-Nov-2000
C;Accession: B70588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-1461 <COL>
A;Cross·references: GB:Z95208; GB:AL123456; NID:g3261747; PIDN:CAB08474.1;
A;Experimental source: strain H37Rv
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, A;Title: Deciphering the biology of Mycobacterium tuberculosi A;Reference number: A70500; MUID:98295987
A;Accession: B70588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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A; Residues: 1-99 <SHI>
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A; Accession: S32700
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nes 73; Conservative
                                                                                                                                                                                                                                                                                                                       74 SYVSMNRVTT-----TGHIVYALKNPVC--LTDAARRPINLLARVEQGLCDVLG----
                                                                                                                                                                                                                                                                                                                                                                                                                  17 PLASAEKSGAYR---HVTRQRALELPYIEANPLVMQSLVITDRDASDADWAADLAGLPSP 73
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                                                                                                                                                                                                                                                                           TLLSPALADTPVQPGIPGRTEVRLDREATAELADAARTRGVTISTLVQMAWATTLSAFTG
                                       WGGPVAEWEHTVFEHIHLLNETI--IADEFATGPLGLNELKHLSRSISRW
                                                                              SYLGENEERAIAGIGEMEDTLLVYENEPPGEVVGTAEFVANGVTE----RPVALESLSHE
                                                                                                                                                                              RGDVTFGVTVSGRPSELSGVETMIGLFINTVPLRVRLDARATVGGQCAVLQRQFAMLRDH
                                                                                                                                                                                                                                                                                                                                                                     PLFVSELLALYRAGGHVAALPAAPRPYRD----YIGWLAGRDQTASRAMWADHLNGLDGP 218
                                                                                                                                                                                                                                 -GDASYGHRITKNP-
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PVTVAAHRSTGELTLLVEVLDGALGTMAPESLGRRVLAVLQRLVSRW
                                                                                                                                    ELRALAHTLDEIHALPEAGN-PRRNV--TRSTVGRNVTLFDTTRMWAYRAVRHS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.1%;
25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 98; DB 2; Length 1461 Pred. No. 8.2;
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Pred. No. 0.17;
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TGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYGHRITKNPLSTAHATLW 143

SGAYRHVTRQRALELPYIEANPLVMQSLVITDRDASDADWAADLAGLPSPSYVSMNRVTT 83

80;

53;

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9;

55; Conser

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84 50 24

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e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushim; y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R. A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6. A; Reference number: A97872; MUID:21429245; PMID:11544234
A; Accession: E97944
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C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revisi
C;Accession: E97944
                                                                                                                                                                                                                                                                      R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamaza DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeor A;Reference number: A72450; MUID:99310339
A;Accession: H72703
                                                                                                                                                                                                                                                                                                                                                                                                                                 probable translation initiation factor eIF-2B APE1047 - Aeropyrum pernix (strain C;Species: Aeropyrum pernix C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE007317; PIDN:AAK99385.1; PID:g15458161; GSPDB:GN00174 C;Genetics:
                                                                                                                A;Cross-references: DDBJ:AP000060; NID:g5104188;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1047
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A; Residues: 1-1876 < KUR>
                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-228 <KAW>
                                                                                                                                                                                                                                                   A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MWAYRAVRHSWGGPVAEWEHTVFEHIHLLNETIIADEFATGPLGLNELKHLSRSISRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ADRNRLIGEPHQWDKLRD---LTEEEKKLPIDSI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENNFYTLHGM---PKNGRYRTEGFDSSYQPVNMM--AGVFGGNTSKSTVGSISFKHNAFR 1738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 6.1%; Score 97.5; D
1 Similarity 19.3%; Pred. No. 13;
46; Conservative 43; Mismatches
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  5.9%; Score 93.5; Di
25.3%; Pred. No. 1.8;
tive 29; Mismatches
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J.; Matsushima,
                                               Length
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, P.; McAhren
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spindle assembly checkpoint protein SLDA - Emericella nidulans (Species: Emericella nidulans, Aspergillus nidulans C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_chang. R;Efimov, V.P.; Morris, N.R. submitted to the EMBL Data Library, November 1997 A;Reference number: 216619 A;Accession: T09224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable ATP/GTP binding protein - Streptomyces coelicolor (fragment) C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 *sequence_revision 03-Dec-1999 *text_change 03-De C;Accession: T37217 R;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M. submitted to the EMBL Data Library, September 1998
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A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-1216 <EFI>
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A; Residues: 1-606 <OLIA
A; Cross-references: EMBL.AL031514; PIDN:CAA20595.1;
A; Experimental source: strain A3(2)
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A;Accession: T37217
A;Status: preliminary; translated
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mes 67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                            RWVWRNFTPETFRARQKAISLRGASKGGKEGGHKGG-----IASGASRRAHTRQQFLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                       RMWAYRAVRHSWGGPV--AEWEHTVFEHIHL-LNETIIADEFATGPLGLNELKHLSRSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAT--LWG--PADALYE---LRALAHTLDEIHALPEAGNPRRNVTRSTVGRNVT-LFDTT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITQQAQLLEEGVPANELVAQ----WDAASSTGTTVKELSSYPAPSLT----LSAAGAVLD 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPVAEWEHTVFEHIHLLNETIIADEFATGPLGLNELK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPADALYELRALAHTLDETHALPEAGNPRRNVTRSTVGRNVTLFDTTRMWAYRAVRHSWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --HLRQSGVNAVVLPDSAAGLAVSRSNAVVFG-ADAAGLDGCLRNKLGTLPLAASAAALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESSWALWAVKPADGVYQWKFTRTAVGADGKVTQSAEA--PGGDIAETDTWVQVTGVFDAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EENNALVLDGSAGYASATGPVVDETGSFTVSARVQLDSAKLASKPVGYEALVAGQQASAG
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Pred. No. 14;
38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from
                                   from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J.; Barrell, B.G.; Rajandream, M.A. September 1998
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                                   GB/EMBL/DDBJ
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                                                                                                                                         #text_change
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A;Title: DNA Sequence of both chromosomes of the cholera A;Reference number: A82035; MUID:20406833 A;Accession: C82199
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A;Introns: 331/3; 477/1
C;Keywords: microtubule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AF032987; NID:g3136093; PID:g3136094
A;Experimental source: strain R153
C;Genetics:
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A; Residues: 1-4558 <HEI>
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Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTX toxin RtxA VC1451 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: C82199
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                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB: AE004223;
                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
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Best Local S
Matches 66
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Best Local Similarity
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                                      2446
                                                                                                        2386 ASKGQPPVKNPKSSASANHKAEWLMTQHAEQWAKITAPYTDNHETLTSTKLASNDKEELH 2445
                                                                                                                                             124
     216
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                                                                                                                                         ASYGHRITKNP------LSTAHATLWGPADALY-----ELRALAHTLDEIH 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LLNETIIADEF --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNVTLFDTTRMWAYRAVRHSWGGPVAEWEHTVFEHIH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DASYGHRITKNPLST-AHATLWGPADALYELRALAHTLDEIHALPEAGNPRRNVTRSTVG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTANRSGSSSLR------VPSPTKDSNP---QGTIIKDTLCNPIDRSIRDTILQELHTT 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLASAEKSGAYRHVTRQRALELPYIEANPLVMQSLVITD-----RDASDADWAAD
 HIHLLNETIIADEFATGPLGLNELKHLSRSISRWVWRNF---
                                    ALGETSNLENNKQQENVASIINTMLNDMLPFYALRTERNLLVQEGDEGFEVRAWPGTEDK 2505
                                                                     ALPEAGNPRRNYTRSTVGR--NVTLFDTTRMWAYRAVRH-----SWGGPVAEWEHTVFE 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERSY---IIRRELGAGAYAPVY------LAESIDNLDSDSEMESVGSNSGRSTVS 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAAYPGYHAHPD-----TQSH--YAPEIERFMKSSSKRSRSGGEAAFDVPIIDPPGG 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAGLPS----PSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETFRARQ 263
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23.6%;
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21.5%;
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                                                                                                                                                                                                                                                                                                                        GB:AE003852; NID:g9655942; O1; strain N16961; biotype
                                                                                                                                                                            Score 89; DB 2;
Pred. No. 2e+02;
90; Mismatches 7
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Pred.
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37;
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                                                                                                                                                                                                               Length 4558
                                                                                                                                                                            Indels
TPETFRARQKAISLR 269
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                                                                                                                                                                                                                                                                                                                        PIDN:AAF94608.1;
El Tor
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H.; Dragoi, :
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I.; Sellers
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R; Andersson, B.; Aslund, L.; Pettersson, U. submitted to the EMBL Data Library, March 1998 A; Description: 93.4 kb of complete sequence from A; Reference number: Z18159 A; Accession: T14611
                                                                                                                                                                                                     RESULT 13
T14611
alanine transaminase homolog - Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Saunders, D.C.: Harris, I
submitted to the EMBL Data
A;Reference number: Z21608
A;Accession: T36509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T36509
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C:Species: Streptomyces coelicolor
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A; Residues: 1-303 <SAU>
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                                     A; Molecule type: DNA
A; Residues: 1-409 <AND>
                                                                    A; Status: preliminary; translated
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Genetics:
                     ;Cross-references:
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                                                                                                                                                                                                                                                                                                                                            EAVAETARKAAALAQRWAE
                                                                                                                                                                                                                                                                                                                                                                               GGIASGASRRAHTROOFLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNPRRNVTRSTVGRNVTLFDTTRMWAYRAVRHSWGGPVAEWEHTVFEHIHLLNETIIADE 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VITDRDA----SDADWAADLAGLPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSFETLFPESWLPRKPLAS---AEKSGAYRHVTRQRAL----ELPYIEANPLV----MQSL 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LARVEQGLCDVLGGDASYGHRITKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEA 168
                                                                                                                                                                                                                                                                                                                                                                                                                  -AKDELGIDLDVDTGILLDLARDAAHGVARPAAPLTTFLVGYAA--
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75; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harris, D.;
                   EMBL: AF052832; NID: g3063540; PID: g3063548; PIDN: AAC14084.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.5%;
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                                                                                                                                                                                                                                                                                                                                            275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              James, K.D.; Parkhill, J.; Barrell, orary, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -PEDAAQHKAIERFILANFDNFEQMPDELFLVDNKVIS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTHVLAQKVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 88.5; DB Pred. No. 6.7;
                                                                            from GB/EMBL/DDBJ
                                                                                                                                 sequence from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -DTW-DDLATARARIREHGHVLDEWISA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107;
                                                                                                                                 Trypanosoma cruzi.
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                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                        199
                                                                                                                                                                                152
291
                             259
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                                                          257
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YNTDTVLASLHSTSKGIIG-ECGRRGGYFCLTNFPAPVREQVLK
                            FRARQKAISLRGASKG--GKEGGHKGGIASGASRRAHTRQQFLE
                                                                                                                                                                              A-SSGVRLLLQ------VLVGDASDAVMVPIPQYPLYTAQLTLLGGTPAMYYLCEKDNW
                                                                                                                                                                                                                                                                                                    RAALATPEGKAKYPFSSIVYCNIGNPQALEQKPLTFFRQVMSLIDA-PFLLENEKVTSQY 91
                                                                                                                                                                                                                                                                                                                                  RKPLASAE-----KSGAYRHVTRQRALE------LPYIEANPLVMQSLVITDRD 57
                                                                                    RHSWGGPVAEWEHTVFEHIHLLNETIIADEFATGPLGLNELKHLSRSISRWVWRNFTPET 258
                                                                                                                                                                                                                                        PADAVARAREYLRHIGDRTGAYTDSAGYAFVRDIVARQINERDHEIKPLVDASSIFLTDG 151
                                                                                                                                                                                                                                                                      ASDADWAA----
                                                                                                                    ALNVEELASVYDECVAKNNATPRVLVVINPGNPTGGVLDRDVMEAVAKFCCDR
                                                                                                                                                ----RALAHTLDEI----HALPEA-----GNPRRNVTRSTVGRNVTLFDTTRMWAYRAV 198
                                                                                                                                                                                                          ARRRPINLLARVEQGLCDVLGGDASYGHR--ITKNPLSTAHATLWGPADALYEL-----
                                                                                                                                                                                                                                                                                                                                                                ;08
                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                          --GIVLMADEVYQENVYAAGKRFLS--FREVVLGL
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                              5.5%;
23.3%;
                                                                                                                                                                                                                                                                    ------DLAGLPSPSYVSMNRVTTTGHIVYAL--KNPVCLTDA 100
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                                                                                                                                                                                                                                                                                                                                                                            Score 87.5;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                Mismatches
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333
                            300
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                                                          PAP 290
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                                                                                                                    256
                                                                                                                                                                              203
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C;Superfamily: nitrogen assimilation regulatory protein ntrC; response regulator homo C;Keywords: DNA binding; nucleotide binding; P-loop; phosphoprotein; transcription re F;5-114/Domain: response regulator homology <RRH>
F;143-36/Domain: RNA polymerase sigma factor interaction domain homology <SFI>F;171-178/Region: nucleotide-binding motif A (P-loop)
F;53/Binding site: phosphate (Asp) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X72382; NID:g313162; PIDN:CAA51075.1; PID:g313166 R;Foster-Hartnett, D.; Cullen, P.J.; Gabbert, K.K.; Kranz, R.G. Mol. Microbiol. 8, 903-914, 1993 A;Title: Sequence, genetic, and lacZ fusion analyses of a nifr3-ntrB-ntrC (A;Reference number: S34980; MUID:93360820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: S03321; S3
R; Jones, R.; Haselkorn,
                                                                                                                                                              A; Gene: ntrC; nifRl C; Superfamily: nitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-457 < KRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Gen. Genet. 215, 507-516, 1989
A; Title: The DNA sequence of the Rhodobacter
A; Reference number: S03318; MUID:89218961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: regulatory protein: C;Species: Rhodobacter capsulatus C;Date: 07-Jun-1990 #sequence_revision C;Accession: S03321; S37299; S34983
                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                  A; Cross-references: EMBL: X72382
                                                                                                                                                                                                                                                                                    A; Molecule type: DN/
A; Residues: 334-449
                                                                                                                                                                                                                                                                                                                                               A; Accession: S34983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data
A; Reference number: S37299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Kranz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X12359; NID:g46077; PIDN:CAA30922.1;
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A; Residues: 1-457 <JON>
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nifR1
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hypothetical protein C - Corynebacterium glutamicum plasmid pGAl C; Species: Corynebacterium glutamicum C; Species: Corynebacterium glutamicum C; Species: Corynebacterium glutamicum C; Apecies: Corynebacterium glutamicum C; Apecies: Corynebacterium glutamicum C; Apecies: Corynebacterium glutamicum C; Apr-1997 #text_change 22-Oct-1999 C; Accession: S60675 M; Hochmannova, J.; Abrhamova, Z. submitted to the EMBL Data Library, August 1995 A; Description: Complete nucleotide sequence of the cryptic plasmid pGAl from Corynebacte A; Reference number: S60673 A; Reference number: S60673 A; Accession: S60673 A; Accession
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Best Local S
Matches 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                       197 RWPLHVSDDPTAYKWHCQHDRVDRLADLMEIART-----MTGSQKPKKYIEQDFSSGRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 KNPLSTAH---ATLW----GPADALYELRALAHTLDEIHALPEAGNPRRNV------ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 APAWIGVNPLSGKCQLIW-LIDPVYAAAGKTSPNMRLLAATTEEMTRVFGADQAFSHRLS 196
                                                                                                                                             311 QLKAAGERLKDAKIIDAYEVAYNVAQAVGADGREPDLPAMRDRLTMARRVRGYVAKG-QP
                                                                                                                                                                                                                                                                                                                                                                          176
370 VVPARRVETQSSRG-RKALATMGRRGAATSNARRWADPESKYAQETRQRLAE 420
                                                                                                                                                                                                                                                                                          251 RIEAAQRATAEAKALAILDASLPSALDASGDLIDGVRVLWINPERARDETAFRHALTVGY 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 ETSRPEG--TDLPLVGRTAAMQALYRLVARVMNADLPVMIMGESGTGKSLIAKAI----H 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385 LRRYF 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 VWRNF 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 DFSDRRTLPFVVAQAADLLGADGPSSLLARRQGRLVVFDEVGDYDDETQGRIVRMLDALP 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 SPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYGHRIT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
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                                                                        ETFRARQKAISLRGASKGGKEGGHKGGIASGASRRA-----HTRQQFLE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAVP-----ALRERVEDIPLLAEHFLGRAERD-----GLGMRAFSAEAMGLVRA-- 324
                                                                                                                                                                                                                                                                                                                                                              ----TRSTV-GRNVTLEDTTRMWAYRA------VRHSWGGPVAEWEHTVFEHI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DASD-----ADWAADLAGLPSPSYVSMNRV-----TTTGHIVY---ALK 92
                                                                                                                                                                                                                     -----HLLNETIIADEF------ATGPLG-----LNELKHLSRSISRWVWRNFTP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETLEPESWLPRKPLA--SAEKSGAYRHVTRQRALELPYI-----EANPLVMQSLVITDR 56
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Search completed: October 4, 2002, 15:35:15 Job time: 127 sec THIS PAGE BLANK (USPTO)

Run OM protein - protein search, October GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. 4, 2002, 15:33:08; using sw model Search time 15.85 Seconds (without alignments) 740.191 Million cell updates/sec

Title: Perfect score: US-09-720-583A-2 1596

Sequence: 1 MDSFETLFPESWLPRKPLAS.....IASGASRRAHTRQQFLEGLS 303

Scoring table: BLOSUM62 Gapop 10.0 ,

Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB : Maximum DB : seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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BL; AIGO765; -; NOT_ANNOTATED_CDS.

BL; AIA132428; -; NOT_ANNOTATED_CDS.

BL; AA475250; -; NOT_ANNOTATED_CDS.

BL; AA498625; -; NOT_ANNOTATED_CDS.

BL; AI386259; -; NOT_ANNOTATED_CDS.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            site-1 protease.
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH)
TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: Under sterol-depleted conditions, SREBPs are cleaved sequentially by site-1 and site-2 protease. The first cleavage occurs within the luminal loop and is directly regulated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: ISOFORM SREBP-1C PREDOMINATES IN LIVER, ADRENAL GLAND, BRAIN AND ADIPOSE TISSUE, WHEREAS ISOFORM SREBP-1A PREDOMINATES IN SPLEEN. BOTH ISOFORMS ARE FOUND IN KIDNEY, THYMUS. TESTIS, MUSCLE, JEJUNUM, AND ILEUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sterol levels.

MISCELLANEOUS: SREBPs have to be in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sterols. The second cleavage by site-2 protease occurs within the first transmembrane stretch and liberates the soluble transcription factor. Cleavage by the cysteine proteases, caspase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activating protein (SCAP) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and caspase-7, is induced during apoptosis, independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P36956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                    PS00038; HELIX_LOOP_HELIX; 1.
                                                                                                                                                                                                                                                                                                                                        metabolism; Nuclear protein; Transmembrane; reticulum; Golgi stack; Alternative splicing.

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P09432;
                                                                                                                                                          operon in Rhodobacter capsulatus.";
Mol. Microbiol. 8:903-914(1993).
-!- FUNCTION: MEMBER OF THE TWO
                                                                                                                                                                                                                            MEDLINE-93360820; PubMed-8355615;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
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01-MAR-1989 (Rel. 10, Last sequence update)
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STRAIN=SB1003;
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                        s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                 . MICROBIOL. 8:903-914(1993).

FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM NTRB/NTRC INVOLVED IN THE ACTIVATION OF NITROGEN ASSIMILATORY GENES SUCH AS GLAA. NTRC IS PHOSPHORYLATED BY NTRB AND INTERACTS WITH SIGMA-54. SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.

SIMILARITY: THE CENTRAL REGION CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                       DNA sequence of the Rhodobacter analogues required for nitrogen Gen. Genet. 215:507-516(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --RRNVTRSTVGRNVTLFDTTRMWAYRAVRHSWGGPVAE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
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Pred. No. 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                       capsulatus ntrA, ntrB and ntrC
fixation.";
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f a nii
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Best Local S
Matches 75
                                                      TKT_RHOCA
Q52723; O68024;
Q52723; O68024;
30-MAY-2000 (Rel. 39
30-MAY-2000 (Rel. 39
16-OCT-2001 (Rel. 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00382; AAA; 1.

SMART; SM00448; REC; 1.

PROSITE; PS0010; RESPONSE_REGULATORY; 1.

PROSITE; PS00675; SIGMA54_INTERACT_2; FAI

PROSITE; PS00688; SIGMA54_INTERACT_3; 1.

PROSITE; PS00688; SIGMA54_INTERACT_3; 1.

PROSITE; PS00688; SIGMA54_INTERACT_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00072; response_reg; 1.
Pfam; PF00158; Sigma54_activat; 1.
                     Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X12359; CAA30922.1; EMBL; X72382; CAA51075.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
            Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                   HSWGGPVAEWEHTVFEHIHLLNET------IIADEFATGPLGL-NELKHLSRSISRW
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                                                                                                                                                                                                                                                                                                                                                                                                             DASD-----TTTGHIVY---ALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETLFPESWLPRKPLA--SAEKSGAYRHVTRQRALELPYI-----EANPLVMQSLVITDR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S03321; S03321.
                                                                                                                                                                                      LRRYF
                                                                                                                                                                                                                                      YAWPGNVRQLENTVRRLVVTASEEEITRTEVEFVLGNQPAVEPLGAGGEGEKLSASIARH
                                                                                                                                                                                                                                                                                                                                      DPPRIMATTQVDLGALMEAGR----RFRQDLYYRLGG---
                                                                                                                                                                                                                                                                                                                                                                                     DFSDRRTLPFVVAQAADLLGADGPSSLLARRQGRLVVFDEVGDYDDETQGRIVRMLDALP
                                                                                                                                                                                                                                                                                                                                                                                                                                     ETSRPEG---TDLPLVGRTAAMQALYRLVARVMNADLPVMIMGESGTGKSLIAKAI----H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fixation; Transcription regulation; Repressor; Activator; ing; ATP-binding; Phosphorylation; Sensory transduction.

1 118 RESPONSE REGULATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR002197; HTH_Fis.
IPR001789; Response_reg.
IPR002078; Sig54_interact.
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                                                                                                                                                                                     389
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143
171
171
425
457
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                                                                                                                        STANDARD;
                                                        . 39, Created)
. 39, Last sequence upo
. 40, Last annotation ucc 2.2.1.1) (TK).
                                                                                                                                                                                                                                                                                      ALRERVEDIPLLAEHFLGRAERD
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343 S
178 A
444 H
50042 MW;
                                                                                                                                                                                                                                                                                                                                                             -CLTDAARRPINLLARVEQGLCDVLGGDASYGHRITKNPLSTAHAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 87; DB 1
Pred. No. 3.3;
28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION (BY SIMILARITY).
SIGMA-54 FACTOR INTERACTION (POTENTIAL)
ATP (POTENTIAL).
H-T-H MOTIF (BY SIMILARITY).
7EB04B4FE4740306 CRC64;
                                                                                                                        PRT;
                                                                                    update)
                                                                                                                        672
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                                                                        update)
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                                                                                                                                                                                                                                                                                    ----GLGMRAFSAEAMGLVRA--
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Matches
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Best Local 9
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PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97404404; PubMed-9256491;
Vloek C., Paces V., Maltsev N., Paces J., Haselkorn R., Fon "Sequence of a 189-kb segment of the chromosome of Rhodobac capsulatus SB1003.";
Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).
-: CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyce 3-phosphate - D-ribose 5-phosphate + D-rylulose 5-phosphate - D-ribose 5-phosphate 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-ATCC 33303 / B10;
MEDLINE-96186907; PubMed-8635754;
Sury D'Aspremont R., Toussaint B., Vignals P.M.;
"Isolation of Rhodobacter capsulatus transketolase:
sequencing of its structural tktA gene.";
Gene 169:81-84(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00801; TRANSKETOLASE_1; 1.
PROSITE; PS00802; TRANSKETOLASE_2; 1.
Transferase; Thiamine pyrophosphate.
CONFLICT 376 382 PETIGGS -> LRNHRRL (IN REF. CONFLICT 484 484 A -> T (IN REF. 1).
SEQUENCE 672 AA; 72436 MW; B6B1E7DE1E66CA80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000360; Transketolase.
Pfam; PF00456; transketolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHATE PATHWAYS.
-!- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
305 KGAAERAEWEARLAALPAG--KRAEFERQMARGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103
                                                                         269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WAADLAGLPSPSYVSMNRV-TTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCD--- 118
                                                                 RGASKGGKEGGHKGGIASGASRRAHTRQQFLEGLS
                                                                                                                                           VDCKTLIGFGSPNKADSYAVHGAPLGDAEIK-LTREAYGWEHGPFVIPAEIKAEWEAIGA
                                                                                                                                                                                                             ---ETII----ADEFAT--GPLGLNELKHLSRSISRWVWRNFT-PETFRARQKAISL
                                                                                                                                                                                                                                                                                               ITIDGRVTVSDVTDQKARFA--
                                                                                                                                                                                                                                                                                                                                                                 STYGRNYTLEDTTRMWAYRAVRHSWGGPVAEWE-----HTVFEHIHLLN------
                                                                                                                                                                                                                                                                                                                                                                                                                                          WVIAGDGCIMEGISQEAIGLAG------KQELDNLIVLWDNNN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -VLGGDASYGHRITKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEAGNPRRNVTR 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WGARMAG--HPEYGHLEGVETTTGPLGQGISTAVGMAIAEK----SMAARFGKKLVDHKI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00456; transketolase; 1.
PF02780; transketolase_C; 1.
PF02779; transket_pyr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF010496; AAC16110.1; -. P23254; ITRK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
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                                                                                                                                                                                                                                                                                       -----ASGWDVLSCDGHDAEDIDRALTAAKKAKRPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
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337
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5-phosphate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74;
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RESULT 4
GUNH_CLOTM

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                                                                                                           Query Match 5.3
Best Local Similarity 22.5
Matches 48; Conservative
                                                                                                                                            ACT_SITE
ACT_SITE
DOMAIN
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REPEAT
SEQUENCE
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P16218;
                                                                                                                                                                                                                                                     Pfam; PF00404; Dockerin_1; 2.
PROSITE; PS00408; EF_HAND; UNNNOWN_1.
PROSITE; PS00448; CLOS_CELULLOSOME_RPT;
PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Gene
                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Clostridium
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01-APR-1990 (Rel.
15-JUL-1998 (Rel.
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                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                 InterPro; IPR002048; EF-hand.
InterPro; IPR001547; Glyco_hydro_F5.
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002105;
                                                                                                                                                                                                                                                                                                                                                               EMBL; M31903; AAA23225.1;
PIR; JH0157; JH0157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-NCIB 10682;
MEDLINE-90323606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1515;
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                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yaguee E., Beguin P., Aubert J.-P.;
"Nucleotide sequence and deletion analysis of the cellulase-encoding
gene celf of Clostridium thermocellum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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110 AGES IN CELLULOSE.

110 AGES IN COTHER C. THERMOCELLUM CELLULOSOME ENZYMES, THIS WELL AS IN OTHER C. THE BINDING LIGAND FOR THE SI COMPONENT.

SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO CELLULAS A (FAMILY 5 OF GLYCOSYL HYDROLASES).

SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 2
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FUNCTION: THIS ENZYME CATALYZES THE ENDOHYDROLYSIS OF FUNCTION: THIS ENZYME CATALYZES THE ENDOHYDROLYSIS OF FUNCTION AND CEREAL
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EYNTVDIKNGKADAYITRMAQDMKAYGKEIWLRPLHEANGD-WYPWAIGYSSRVNTNETY
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(EC 3.2.1.4) (EGH)
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CATALYTIC (BY SIMILARITY).
PRO/THR-RICH (LINKER).
PRO/THR-BICH (LINKER).
CELLULOSE-BINDING (BY SIMILARITY).
PRO/TON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
2 X 24 AA APPROXIMATE REPEATS.
                                              Score 85; DB
Pred. No. 12;
6; Mismatches
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Maccarthy A.B., Sloane-Stanley J., Buckle V.J., Kearney L.,
Higgs D.R., Ratcliffe P.J., Harris P.C., Roelfsema J.H.,
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P98161;
VARIANTS
F-4190.
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01-OCT-1996 (Rel. 34,
01-MAR-2002 (Rel. 41,
                                                                                                                                                              MEDLINE=96108969; pubMed=8:
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                                                                                                                                                                                                                                                               "The structure of a PKD domain polycystic kidney disease."; EMBO J. 18:297-305(1999).
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                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMK OF 2,0 0-1889186;
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Rateman A., Clarke J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 2769-4303
MEDLINE-94273192; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gluecksmann-Kuis M.A., Tayber O., Woolf
Deng N., Alperin G.D., Iris F., Hawkins
Duyk G., Schneider M.C., Geng L., Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=95254638; PubMed=7736581;
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Mammalia; Eutheria;
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                                                                                                                                                                                     ADPKD 3748-ARG--VAL-3752 DEL, =96108969; PubMed=8554072;
                        ADPKD
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; Metazoa; Chordata; C
""+heria; Primates; (
                                                                                 Harris P.C.;
the 3' region of the polycystic
'~ a'v novel mutations.";
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PubMed=8004675;
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58:86-96(1996).
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Hawkins F., Munro (
., Zhang F., Zhao Z
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AEDLINE-9/34622...

Peral B., Gamble V., Strong C.,

Zerres K., Winearls C.G., Harris P.C.,

"Identification of mutations in the duplicated region

polycystic kidney disease 1 gene (PKD1) by a novel app

polycystic kidney disease 1 gene (PKD1) by a novel app

""" Genet. 60:1399-1410(1997).
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                                                                                           Watnick T., Phakdeekitcharoen B.,
Briefel G., Klinger K.W., Klinberl.
"Mutation detection of PKDI ident
three families with aneurysms and
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                                                                                                                                                                                                                        Thomas R.L.,
Sandford R.;
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                                                                                                                                                          VARIANTS ADPKD
                                                                                                                                                                                                  dominant polycystic
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=97403939; PubMed=9259200;
.E., Rossetti S., Bresin E
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, Lens X.
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stic kidney disease
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lontek K.B., Corda
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VARIANTS ADPKD Q-13; F-75; C-139; 1992-F-T-1993 2224 DEL; D-2336; D-2752; 2762-ILMR-2765 DDPL; M S-2858; 3012-T-Y-3017 DEL AND 3752 DE 2674; M-2708; T-2734; L-2735; C-2765; M-2782; R-D-2966 AND L-3066. MEDLINE-21063179; PubMed-11115377; MEDLINE-21063179; PubMed-11115377; Rossetti S., Strmecki L., Gamble V., Burton S., Roy S., Bakkaloglu A., Komel R., Winearls C.G., Mutation analysis of the entire PKD1 gene: gene
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MEDLINE-20467506; Pubmed-11012875;
Phakdeekitcharoen B., Watnick T.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS ADPKD GLN-3719 AND PRO-3852, MEDLINE-20514565; PubMed-11058904; Aquiari G., Savelli S., Garbo M., Bozz
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Harris P.C., Deltas C.O
"Screening of the PKD1
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MEDLINE=20311156; PubMed=10854095;
Mercier B., Quere I.,
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AND LEU-3193.
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Jul AND MET-3375, A
L, Mean R., Demetriou K., Composition C.C.;
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kidney disease families.";
. 16:176-176(2000).
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J. Virol. 55:387-394(1985).
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                                                                                                            69; Conser
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                                                                                                                                                                                                                                                                                                                                                                                ; IPR003308; Integ; IPR002156; RNase; IPR000477; RVTse; IPR001584; Rve.
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i (Rel. 02, Last sequence update)
i (Rel. 40, Last annotation update)
i polyprotein [Contains: Endonuclease;
use (EC 2.7.7.49)].
                                                                                                                                                                                                           RNA-directed DNA polymerase; Hydrolase; Nuclease; Polyprotein.
363 AA; 97036 MW; 704AEF7FC6BlD886 CRC64;
                                                                                                            Conservative
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01-FEB-1995 (Rel. 3
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-I- SUBCELLULAR LOCATION: NASCENT ACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93183503; PubMed=8442953;
Freemerman A.J., Wright R.M., Flickinger C.J.,
"Cloning and sequencing of baboon and cynomolgu
acrosomal protein SP-10: homology with human SP
antigen (MSA-63).";
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SHORT FORM; ARE PRODUCED BY ALTERN
-i- TISSUE SPECIFICITY: TESTIS.
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                                                                                                                                                                                 opean Bioinformatics Institute. There are no rest non-profit institutions as long as its content dand this statement is not removed. Usage by an srequires a license agreement (See http://www.isb-an email to license@isb-sib.ch).
                                                                                                 Glycoprotein;
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MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch
Riley M., Collado-Vides J., Glasner J.
Gregor J., Davis N.W., Kirkpatrick H.A
                                                                                                          STRAIN-HB101;
STRAIN-B101; PubMed-1769955;
MEDLINE-92121142; PubMed-1769955;
Mau B., Shao Y.;
"The complete genome sequence Science 277:1453-1474(1997).
                                                                             Kanatani A., Masuda T., Shimoda T., Yoshimoto T., Tsuru D.;
"Protease II from Escherichia coli: enzyme gene and characterization of J. Blochem. 110:315-320(1991).
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InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR001375; Peptidase_S9.
InterPro; IPR004106; Peptidase_S9_N.
InterPro; IPR002471; Prol_endopep_ser.
InterPro; IPR002471; Prol_endopep_ser.
InterPro; IPR002470; Proligo_PTase.
Pfam; PF00326; Peptidase_S9; 1.
Pfam; PF00326; Peptidase_S9_N; 1.
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SEQUENCE FROM
STRAIN-K12;
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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InterPro; IPR000477; RVTse.
InterPro; IPR001584; Rve.
pfam; PF00552; Integrase; 1.
pfam; PF02022; Integrase_Zn; 1
pfam; PF00075; rnaseH; 1.
pfam; PF00078; rve; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-86286596; PubMed-3016667;
Ymer S., Tucker W.Q.J., Campbell H.D., Young I.G.;
"Nucleotide sequence of the intracisternal A-particle genom
5 to the interleukin 3 gene of the leukemia cell line WEHI
Nucleic Acids Res. 14:5901-5918(1986).
-i- MISCELLANEOUS: THIS PARTICLE IS A DEFECTIVE RETROVIRUS.
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P12894;
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Mouse intracisternal a-particle (IAP-IL3).
Viruses; Retroid viruses; Retroviridae; Intracisternal A-particles.
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01-NOV-1995 (Rel.
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4 AA; 91000 MW; A369620A450F729A CRC64;
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cell line WEHI-3B.";
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RESULT TO A CONTROLL TO A CONT
TIGR; MT4410;
Tuberculist; Rv2157c; -.
InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
Pfam; PF01225; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase_C; 1.
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harr:
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyo
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
UDP-N-acetylmuramoylalanyl-D-gluttamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase (EC 6.3.2.15) (UDP-MurNAc-pentapeptide synthetase)
(D-alanyl-D-alanine-adding enzyme).
MURF OR RV2157C OR MT2216 OR MTCY270.11.
                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: INVOLVED IN CELL WALL FORMATION. CATALYSES THE FI
STEP IN THE SYNTHESIS OF UDP-N-ACETYLMURAMOYL-PENTAPEPTIDE,
                                                                                                                                                                                         EMBL; 295388; CAB08670.
EMBL; AE007068; AAK4650
HSSP; P11880; 1GG4.
TIGR; MT2216;
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STRAIN-CDC 1551 /
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SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR IOCATION: Cytoplasmic (Probable).
SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s requires a license agreement (See http://www.isb-sib.an email to license@isb-sib.ch).
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                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation. European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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RESULT 12
RADA_PSEAE
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Best Local Similarity
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PROSITE; PS5017
Cell adhesion;
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Smith K.A., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
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                                                                                                                       STRAIN-FRD1;
Howell M.L., Heur M.,
"Pseudomonas aeruginos
                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
DNA repair protein radA homolog (DNA repair
RADA OR SMS OR PA4609.
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REPEAT
                                                                                                                 Submitted
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                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                         SEQUENCE FROM
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                                                                                                                                                                                           Pseudomonas
                                                                                                                                                                                                    Bactería; Proteobactería;
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                                                                                                              nas aeruginosa
(MAR-1997) to
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                                                                                                                                                                                                              aeruginosa
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                                                                                                                                    Klotz M.G.,
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                                                                                                             M.G., Hassett D.J.;
dative stress operon.";
EMBL/GenBank/DDBJ data
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Pred. No. 18;
36; Mismatches
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RESULT 13
SPCQ_HUMAN
ID SPCQ_H
AC Q9H254
AC Q9H254
DT 01-MAR
DT 01-MAR
DT 01-MAR
CT 01-MAR
DT 01
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Best Local S
Matches 62
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CONFLICT
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CONFLICT
SEQUENCE
                                                              09H254: 09HCDO; Q9H3G8; Q9H1K7; Q9H1K8; Q9H1K9; 01-MAR-2002 (Rel. 41, Created) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) 01-MAR-2002 (Rel. 41, Last annotation update) Spectrin beta chain, brain 3 (Spectrin, non-erythroid beta chain (Beta-IV spectrin).

SPTBN4 OR SPTBN3 OR KIAA1642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U89384; AAB49466.1; -. EMBL; AE004875; AAG07997.1; -. InterPro; IPR003593; AAA. InterPro; IPR001984; Lon_endopep. InterPro; IPR001553; RecA.
                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit modified and this stentities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence opportunistic pathogen."; Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA repair;
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
                                                 Homo sapiens (Human)
                                                                                                                                                                               SPCO_HUMAN
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-!- SIMILARITY: BELONGS TO THE RADA FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bioinformatics Institute. There are no restropy by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                          DEIHALPEAGNPRRNVTRSTVGRNVTL-FDTTRMWAYRAVRHSWGGPVAEWEHTVFEHI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPRVLEHMVDTVLYFEGESDGRLRLLRAVKNRFGAVNELGVFGMTDKGLKEVSNPSAI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPLVMQSLVITD-RDASDADWAADLAGLPSPSYVSMNRVTTTGHIVYALK---NPVCLTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDSFETLFPESWLPRKP------LASAEKSGA----YRHVTRQRALELPYIEA 43
                                                                                                                                                                                                                                                               GGVKVLETASDLALMAAVMSSLRNRPLPHDLLVFGEVGLS 397
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62; Conser
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96
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                                                                                                                                                                               STANDARD;
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C4-TYPE (POTENTIAL).
ATP (POTENTIAL).
E -> K (IN REF. 1).
E -> D (IN REF. 1).
GR -> AA (IN REF. 1).
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Pred. No. 10;
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               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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F (IN REF. 1).
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Pfam; PF00307; CH; 2.

Pfam; PF00435; PH; 1.

Pfam; PF00435; Spectin; 18.

PRINTS; PR00683; SPECTRINPH.

SMART; SM00033; CH; 2.

SMART; SM00133; PEC; 16.

SMART; SM00120; SPEC; 16.

PROSITE; PS00020; ACTININ_1; 1

PROSITE; PS00020; ACTININ_2; 1
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EMBL; AF082075; AAG38874.1;
EMBL; AY004226; AAF93171.1;
EMBL; AY004226; AAF93172.1;
EMBL; AY004227; AAF93173.1;
EMBL; AY004227; AAF93173.1;
EMBL; AB046862; BAB13468.1;
MIM; 606214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001715; (InterPro; IPR001849; InterPro; IPR002017; (InterPro; IPR001605; IP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Hermel J.-M., Zhang J.-P., Philbrick W., Slepnev
Solimena M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. [2]
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"A new spectrin, beta-IV, has a major truncated isoform associates with promyelocytic leukemia protein nuclear b nuclear matrix.";
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SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-21316449; PubMed-11294830;
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                                                                                                                                   Alternative
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European Bioinformatics Institute
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SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY
SIMILARITY: CONTAINS 1 PH DOMAIN.
SIMILARITY: CONTAINS 18 SPECTRIN REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the EN
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PS50003;
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                            ACTIN-BINDING CH 1.
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Methionine aminopeptidase (EC 3.4.11.18) (MAP)
MAP OR MTH1296.
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                 Methanobacterium thermoautotrophicum
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22.3%;
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RDGTCL (...
MISSING (IN
MISSING (IN REF. 2...
E -> K (IN REF. 2...
E -> K (IN REF. 1).
G -> S (IN REF. 1).
71.5; DP
91.
         Methanobacteriales;
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SPECTRIN 18.

PH.

MISSING (IN ISOFORM 3).

AVQAAEGLLRQGNIYGEQAQEAVTRLLEK -> MPHYPSCS
SAPSIGTPIPPQIQULEARHR (IN ISOFORM 3).

NQENQLRAQQMQKLHDQLELQH -> CLIIHPALLHPPWE
PPYLPRSSS (IN ISOFORM 2).

MISSING (IN ISOFORM 2).
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Pred. No. 91;
38; Mismatches
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A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
A Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
A Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
A Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
A McDougall S., Shiner G., Goyal A., Pietrovski S., Church G.M.,
A Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH; functional analysis and comparative genomics.";
J. Bacteriol. 179,7135-7155(1997).
C. -!- FUNCTION: REMOVES THE ANINO-TERMINAL METHIONINE FROM NASCENT
C. -- CATALYTIC ACTIVITY: L-METHIONYLPEPTIDE + H(2)0 = L-METHIONINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                   ENTC_ECOLI STANDARD; PRT; 391 AA. P10377; P77099; 01-MAR-1989 (Rel. 10, Created) 01-OCT-1994 (Rel. 30, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) 150chorismate synthase entc (EC 5.4.99.6). ENTC OR B0593 OR Z0735 OR ECS0632. EScherichia coli, and Ecscherichia coli, and Ecsc
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SEQUENCE
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InterPro; IPR002468; MAP_2.
InterPro; IPR001714; Methamino_PTas;
InterPro; IPR000994; Peptidase_M24.
Pfam; PF00557; Peptidase_M24; 1.
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Pred. No. 7.2;
9; Mismatches
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SEQUENCE FROM N.A.

STRAIN=0157:H7 / RIMD 0509952;

MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Y.

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., T.

11da T., Takami H., Honda T., Sasakawa C., Ogasawara N., Ya

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

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0157:H7 and genomic comparison with a laboratory strain K-1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
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SEQUENCE FROM N.A.
Allen E.,
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"Nucleotide sequence of Escherichia coli isochorismate synthetase
gene entc and evolutionary relationship of isochorismate synthetase
and other chorismate-utilizing enzymes.";
13. Bacteriol. 171:775-783(1989).
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Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Le
Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gregor J., Davis N.W., Kirkpatrick H.A.,
Mau B., Shao Y.;
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Elkins M.F., Earhart C.F.;
"Opacity factor from group A streptococci
FEMS Microbiol. Lett. 56:35-40(1988).
                                                                                                                           PARTIAL SEQUENCE,
MEDLINE-90241936;
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MEDLINE=97426617; Pu
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ol. Biol. 212:669-682(1990).
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Search completed: October 4, 2002, 15:36:31 Job time: 203 sec

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Best Local Similarity
Matches 98; Conserv
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030683;
01-JAN-1998
01-JAN-1998
01-DEC-2001
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01-MAY-1999
01-DEC-2001
                                                                                                                                                                            PUTATIVE REPA.
MEDLINE-98015402; PubMed-9353918;
De Mot R., Nagy I., De Schrijver A., Patt Schoofs G., Vanderleyden J.;
"Structural analysis of the 6-kb cryptic Rhodococcus erythropolis NI86/21 and cons Rhodococcus shuttle vectors.";
Microbiology 143:3137-3147(1997).
                                                                                SEQUENCE FROM N.A. STRAIN=NI86/21;
                                                                                                                 Actinomycetales;
NCBI_TaxID=1833;
                                                                                                                                       Plasmid pFAJ2600.
Bacteria; Firmicutes;
                                                                                                                                                              Rhodococcus erythropolis.
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EMBL; AJ007958; CAA07792.1; -.
InterPro; IPR004322; Replicase.
Pfam; PF03090; Replicase; 1.
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plasmid pT3.2I.
Bacteria; Proteobacteria;
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998 (TrEMBLrel. 05, Last sequence up
001 (TrEMBLrel. 19, Last annotation
REPLICATION PROTEIN.
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Pred. No. 3.6e-22;
0; Mismatches 129;
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Best L
  Query Match
Best Local
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                                                                            "Cloning and DNA sequence of the plasmid pAL5000."; Plasmid 27:130-140(1992). EMBL; M23557; AAA98171.1; -EMBL; M60875; AAA25372.1; -InterPro; IPR004322; Replicase.
                                             Plasmid.
SEQUENCE
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SEQUENCE
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                                                                                                                                                SEQUENCE OF 160-336 FROM N.A. MEDLINE=92311251; PubMed=1615063; Labidi A., Mardis E., Roe B.A., W
                                                                                                                                                                                    Gene 71:315-321(1988).
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=89138007; PubMed=3224826;
Rauzier J., Moniz Pereira J., Gic
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NCBI_TaxID=1766;
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SEQUENCE FROM N.A.
MEDLINE-95050306; PubMed-7525540;
MEDLINE-95050306; PubMed-7525540;
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7; Mismatches 121;
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Bacteria; Proteobacteria; Shigella.
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InterPro; IPR004322; Replicase.
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                                                                                                                                                                                                                                                                                                                       SIAKYTHRNFTPETF-AQYVATTHTPEIQAAR--GRKGGIAKGAGYEDKRSTALEMLVNG
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Pred. No. 2.5e-20;
3; Mismatches 124;
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Q51639;
Q51-NOV-1996
  Plasmid.
SEQUENCE
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SEQUENCE
                                              InterPro; IPRO(Pfam; PF03090;
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Escherichia
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Plasmid ColE9-J.
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                                                                   J. Bacteriol. 176:7233-7243(1994).
EMBL; D30064; BAA06302.1; -.
InterPro; IPR004322; Replicase.
InterPro; IPR001440; TPR.
                                                                                                                                                                                                     MEDLINE-95050306; Pu
Hiraga S., Sugiyama
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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EMBL; D30061; BAA06299.1; -.
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"Comparative analysis of
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InterPro; IPR001440; TPR.
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Comparative analysis of the replicon
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    34851 MW;
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  2245A0EA06FBF085 CRC64;
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Query Match Best Local S Matches 90

Similarity

19.8%;

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Conservative

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Score 316.5; DB : Pred. No. 6.9e-20; 8; Mismatches 124

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01-OCT-2000
01-OCT-2000
01-DEC-2001
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Hirasawa K., Ishii Y., Kobayashi M., Koizumi K.,
"Improvement of Deulfurization Activity in Rhodoc
KA2-5-1 by Genetic Engineering.";
Biosci. Biotechnol. Biochem. 65:239-246(2001).
EMBL: AB040101; BAA92818.1; -.
InterPro; IPR004322; Replicase.
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IAASIHRWIVTKSRMWAD-GPAVYEATFVAIQSARGRKMTEKK--
                                              LSRSISRWV-----
                                                                                               CMLFETARTWAYRELRCHWGDP-----
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                                                                                                                                                                                                                                                                                             NHPLPNATVENPRNGHAHAVWALTEPFTRTEYARRKPLAYAAAVNEGLRRAVDGDAAYSG
                                                                                                                                                                                                                                                                                                                                        -LPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYGH
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                                              WRNFTPETFRARQKAI-SLRGASKGGKEGGHKGGIASGASRRAHT
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Last annotation update)
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Pred. No. 1.9e-19;
1; Mismatches 115;
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SEQUENCE
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SPECIES-P.jensenii; STRAIN-DFI; PIASMID-
Stierli M.P., Meile L., Teuber M.;
"Molecular analysis of plasmid pLME106,
Propionibacterium jensenii.";
Submitted (OCT-1999) to the EMBL/GenBan)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium jensenii, and Propionibacterium acidipropionici. Plasmid pLME106, and Plasmid pRG01. Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Propionibacterineae; Propionibacterium.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
PUTATIVE THETA REPLICASE (REPLICATION PROTEI
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01-OCT-2000
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Yamashita M., Murooka Y.;
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                                                                                                                                                               LNELKHLSRSISRWVWRNF------TPETFRARQKAISLRGASKGGKEGGHKG-GIA
                                                                                                                                                                                                                GRNCALFETARTWAYRDARRIRORHEY -- PTAEDSADLHAVIASTVEALNAG--YSEPLP
                                                                                                                                                                                                                                                           GRNVTLFDTTRMWAYRAV-----RHSWGGPVAEWEHTVFEHIHLLNETIIADEFATGPLG
                                                                                                                                                                                                                                                                                                               DASYAGLITKNPEHPAWNTTW-CTDHLYRLAELDTHLDAAGLMP-APSWRRTRRRNPYGL
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                                                                                                                 AREAAGIAASIHRWITHRFYGWIDSHTVNEATFSTIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 306;
Pred. No. 5.
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Propionibacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
.6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piao Y.Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
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                                                                                                                 -SYR-
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287

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183

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                            Escherichia coli.
Plasmid ColE2imm-K317.
Bacteria; Proteobacteria;
                                                                                        Q51632;
01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid 36:36-41(1996).
EMBL; U39878; AAB03568 1;
InterPro; IPR004322; Replicase.
Pfam; PF03090; Replicase; 1.
Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TREMBLIFEL 01, C
01-NOV-1996 (TREMBLIFEL 01, L
01-DEC-2001 (TREMBLIFEL 19, L
PLASMID PRBL1 PUTATIVE THETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q45279
Q45279;
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Ankri S., Bouvier I., Reyes O., Predali
"A Brevibacterium linens pRBL1 replicon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid autonomous circular plasmid pRBL1.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Micrococcineae; Brevibacteriaceae; Bre
NCBI_TaxID-1703;
 SEQUENCE FROM N.A
                     NCBI_TaxID=562;
                                   Escherichia
                                                                                 REP PROTEIN.
                                                                                                                                          Q51632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brevibacterium linens
                                                                                                                                                                                                   285
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                                                                                                                                                                                                             KGGIASGASRRAHTRQQFLEGLS
                                                                                                                                                                                                                                               GMNSTFSEALPASEIRATIRSFYKWITTRYTGWLDSRTTSQSKSAAYHRNT--
                                                                                                                                                                                                                                                                                            TKRKNPV--GLGRNCTLFETVRWDVYRVARTI----RKRNEHPTPEDRHDLEAAIVNLCQ
                                                                                                                                                                                                                                                                                                                                         TEGLRRSVDGDKGYSGLITKNPTHDQWEASW-LTDHLYNLDELTEHLTVSDFMPPDSWQR
                                                                                                                                                                                                                                                                                                                                                                                       LMRAMWNRKAW------QPNAVVENPANGHAHAVWALAEPVTRTEYARRKPLAYAAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFETLFPESWLPRKPLASAE-KSGAYRHVTRQRALELPYIEANPLVMQSLVITDRDASDA
                                                                                                                                                                                                                                                                                                                  NPRRNVTRSTVGRNVTLFDTTRMWAYRAVRHSWGGPVAEWEHTVFEHIHLLNETII----
                                                                                                                                                                                                                                                                                                                                                                EQGLCDVLGGDASYGHRITKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                    STET-WGQMWLPLWPLASDDLLQGIYR-TSRHNALELRYIEANPQSLSNLLVVDIDHPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106;
                                                                                                                                                                                                  KGGVVSGQVR----RQKALERVS
                                                                                                                                                                                                                                                                     -ADEFATGPLGLNELKHLSRSISRWVWRNFT----PETFRARQKAISLRGASKGGKEGGH 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  ----DWAADLAGLPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.0%;
nilarity 32.8%;
Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 AA;
                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35266 MW;
                                                                                            01,
19,
                                              gamma
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Last annotation update)
A REPLICASE (ORF310).
                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 304; DB
Pred. No. 8.8e-
34; Mismatches
                                                                                                                  Created)
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                                                                                                                                                                                                  303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3DB4DF1F26A98BF4 CRC64;
                                              subdivision;
                                                                                                                                         311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F., Leblon functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
.8e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137;
                                              Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brevibacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium
                                                                                                                                                                                                                                               -GRKGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46;
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Best Local S
Matches 90
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q51630;
Q51630;
01-NOV-1996
01-NOV-1996
01-DEC-2001
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Pfam; PF03090;
Plasmid.
SEQUENCE 311
                                                                                                                                                                                                                                                                      Plasmid.
SEQUENCE
                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 176:7233-7243(1994).
EMBL; D30056; BAA06294.1; -
InterPro; IPR000792; HTH_LuxR.
InterPro; IPR004322; Replicase.
Pfam; PF03090; Replicase; 1.
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EMBL; D30058; BAA66296.1; -.

InterPro; IPR000792; HTH_LuxR.

InterPro; IPR004322; Replicase.

InterPro; IPR001440; TPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-95050306; PubMed-7525540;
Hiraga S., Sugiyama T., Itoh T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REP PROTEIN.
Escherichia coli.
Plasmid ColE2-CA42.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmids."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmids.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Comparative analysis of the replicon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hiraga S., Sugiyama T., 1
"Comparative analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128
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FPESWLPRKPLASAEKSGAYRHVTRQRALELPYIEANPLVMQSLVI--TDRDASDADWAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HRITKNPLSTAHATLWGPADALYELRALAHTLDEI-HALPEAGNPRRNVTRS-TVGRNVT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EENLPHRPYHTDDLAFGLRISGKGRALLARYIQQNQPHAQFWLVFDVDREGAAIDWSDRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAKYTHRNFTPETF----AQYVADTHTPETQAKRGRKGGTAKG----EAYDDKRFM
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                                                                                                  25 19.0%; Similarity 30.4%; 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 68
                                                                                                                                                                                                                                                                      311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176:7233-7243(1994).
                                                                                                                                                                                                                                                                      A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Replicase; 1.
                                                                                                                                                                                                                                                                      35298 MW;
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01,
19,
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f the
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                                                                                                         55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created
                                                                                               Score 303; DB 2;
Pred. No. 1.1e-18;
5; Mismatches 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 303.5; DB 2
Pred. No. 9.8e-19;
3; Mismatches 125
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Q9RLE8;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE REPLICON PROTEIN.
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Plasmid 45:88-100(2001).
EMBL; AJ249644; CAB56518.1; -.
InterPro; IPR004322; Replicase.
Pfam; PF03090; Replicase; 1.
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MEDLINE-21223402; PubMed-11322823;
Avison M.B., Walsh T.R., Bennett P.M.;
"pUB6060: a broad host-range, DNA polymerase-I-independent ColE2-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid p11184.
Bacteria; Proteobacteria;
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177 CHLFEMTRKWAYRAIRQGWPA-FSQWLDAVIQRVEMYNASLPV------PLSPPECRAIG 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 YSGLICKNPFHLE----W----QVMEWREEAYTLDELADYLDLSTSARRSIDKHYGMGRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 TLENDR-LPHKPYFSDDLQFGVRIAGKERALLAKYIQFNQPHAMYWLCFDVDRAGAAIDW 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 TLFPESWLPRKPLASAEKSGAYRHVTRQRALELPYIEAN-PLVMQSLVI-TDRDASDADW 63
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                                                                    IAKSISKWTMVTYRSLGFDEYVKLTHSPEVQAYRGRRSKGGGRPSIGEPWLALGISRRSY
                                                                                                                                        LSRSISRWV-----WRNFTPETFRARQKAISLRGASKGGKEGGHKGGIASGASRRAH 293
                                                                                                                                                                                                                RNCTLFDKTRKWAYRAIROGW-PEYSQWLQACIERAKAYNLQFSA-----PLDENEVMG
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Gapop 10.0 , Gapext 0.5
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US-08-658-136-5

US-08-1460-751-2

US-08-191-879-2

US-08-928-361B-30

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US-08-928-361B-6

US-08-928-361B-6

US-08-92-045-5

US-09-055-474-33

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US-08-947-965-74

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US-08-99-11-730-1

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72.5	72.5	72.5	72.5	72.5	72.5	72.5	73.5	73.5	74	74	74	74.5	75	75	75	75	75
4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.6	4.6	4.6	4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.7
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US-08-804-227C-5	US-08-860-339-18	US-08-481-435-10	US-08-481-435-2	US-09-079-630-32	US-08-577-492-32	US-08-737-825-9	PCT-US92-06965A-25	US-08-867-611-20	US-08-672-564-1	US-08-672-564-9	US-08-292-045-7	US-08-943-714-2	US-08-928-361B-5	US-08-928-361B-11	US-08-938-365-2	us-09-500-569-10	US-09-216-295-14
5, A	Sequence 18, Appl	Sequence 10, Appl	Sequence 2, Appli	Sequence 32, Appl		Sequence 9, Appli	Sequence 25, Appl	Sequence 20, Appl	Sequence 1, Appli	Sequence 9, Appli	Sequence 7, Appli	Sequence 2, Appli	Sequence 5, Appli	Sequence 11, Appl	Sequence 2, Appli	Sequence 10, Appl	Sequence 14, Appl

ALIGNMENTS

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; Sequence 5, Application US/08658136
Patent No. 6071717
; GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
; LENGTH: 4302 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-658-136-5
                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: LASSEM, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELEPHONE: 508-872-8400
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 5:
INFORMATION FOR SEQ ID NO: 5
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APPLICANT: GERNINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: ONE MOUNTAIN CITY: FRAMINGHAM STATE: MASSACHUSETTS COUNTRY: USA
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Matches Query Match Best Local Similarity Conservative 5.3%; Score 84.5; 21.1%; Pred. No. 26; Mismatches 111; DB Length 4302; Indels 75; Gaps

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; TOPOLOGY: unknown ; MOLECULE TYPE: protein US-08-460-751-2
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Sequence 2, App...
Sequence 2, App...
                                                              Query Match
Best Local
                                                Matches
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                                                                                                                                                                                                                                                                   TELEFAX: (212) 869-886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Glucksma
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                       TYPE: amino acids
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STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/460,751 FILING DATE: 02-JUN-1995 CLASSIFICATION: 435
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  4 FETLFPESWLPRKPLASAEKSGAYRHV--
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                                            Similarity 21.1 59; Conservative
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Reeders, Stephen
Schneider, Michael
Schneider, Michael
Glucksmann, Sandra
                                                                                                                                                                                                                                                                                                                                      (212) 869-8864/9741
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                                                                5.3%;
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                                       Score 84.5; DB 2;
Pred. No. 26;
5; Mismatches 111;
----TRQRALELPYIEANPLVMQSLVI 53
                                                                                     Length 4303;
                                            Indels
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                                       Gaps
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; SEQ ID NO 2; LENGTH: 450; TYPE: PRT; ORGANISM: Streptococcus pneumoniae US-09-191-879-2
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APPLICANT: Chalker, Alison F.
APPLICANT: Chalker, Alison F.
APPLICANT: Mazulla, Marie J.
TITLE OF INVENTION: DnaB
FILE REFERENCE: GM10183
CURRENT APPLICATION NUMBER: US/09/191,879
CURRENT FILING DATE: 1998-11-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.2%; Score 83.5; DB 4; Best Local Similarity 22.2%; Pred. No. 0.97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jaworski, Deborah |
APPLICANT: Wang, Min
APPLICANT: Warren, Richard L.
APPLICANT: Lennox, Anna L.
APPLICANT: Ingraham, Karen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 7 SOFTWARE: FastSEQ for Windows Version
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                                          210
274 QKYTIAQGNLANASIYIDD--TPGIRITEIRSRSRKLAQ 310
                                                                                                                                                                           155 NRSGFKNIRDVLNLNFGNLEARSQOTTDITGIATGYRDLDHMTTGLHEEELIILAARPAV 214
                                                                                                                                                                                                                      124 ASYGHRITKNPLSTAHATLWGPADALYEL------RALAHTLDEIH------ALPEA 168
                                                                                                                                                                                                                                                                       97
                                                                                                                                                                                                                                                                                                               37 YIESRDEFKYAHRLIFQAMVDLSDRGDAIDATTVRTILDNQGDLQNIGGLSYLVEIVNSV 96
                                                                                                                                                                                                                                                                                                                                                                                                      40 YIE-----ANPLVMQSLV-ITDR-DASDA-----DWAADLAGLPSPSYV--SMNRV 81
                                       EHTVFEHIHLLNETIIADEFATGPLGLNELKHLSRSISR 248
                                                                                  GKTAFALNIAQNI-GTKLDKTVAIFSLEMGAESLVDRMLAAEGLVESHSIRTGQLTDEEW 273
                                                                                                                                 G-----NPRRNVTRSTVGRNVTLFD-----TTRMWAYRAVRHSWG---GPVA--EW 209
                                                                                                                                                                                                                                                                  PTSANAEYYAK - - IVAEKAMLRRLIAKLTESVNQAYEASQPADEIIAQAEKGLIDVSENA 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --LWDLGDGGWLEGPEVTHAYNSTGDFTVRVAGWNEVSRSEAWLNVTVKRRVRGLV---- 1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGLCDVLGGDASYGHRITKNPLSTAHATL-------WGPADALYELRALAHTLD 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Mismatches
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US-08-928-361B-30
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Verny, Hand
REGISTRATION NUMBER: 30,518
REFERENCE, DOCKET NUMBER: 480.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-324-1678 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/928,361B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                               615
                                                                                                                                                                                                 512
 658
                               257
                                                                                                202
                                                                                                                                 560
                                                                                                                                                                145
                                                                                                                                                                                                                                                              452 VVPDEEAKDQADKGKDGLIVPPTNSINKDPVTNTQYSNTTGNIINPETGKVIPGSLPGSL 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  89
                                                                                                                                                                                                                                                                                               52 VITDRDASD-ADWAADLAGLPSPSYVSMNRVT-----TTGHIV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/026,062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                             ETFRARQKAISLRGASKG-----GKEGGHKGGIASGASRRAHTRQQFLEGLS 303
                                                                                             WGGPVAEWEHTVFEHIHLLNETIIADEFATG-PL----GLNELKHLSRSISRWVWRNFTP 256
                                                                                                                                                               PADALYELRALAHTLDEIHALP---EAGNPRRNVTRSTVGRNVTLFDTTRMWAYRAVRHS
                                                                                                                                                                                               NYPSFNTPQQTDEITGKPVDTVTG-----LPYDPSTGEIIDPATKLPIPGSVA----
                                                                                                                                                                                                                             -YALKNPVCLTDAARRRPINLLARVEQGLCDVLGGDASYGHRI---TKNPLSTAHATLWG
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                                                                                                                              -GDEIL-TEVLNITTDEVTGLPIDLETGLPRDPVSGLPQLPNGTLVDPSNK---KPIPGS
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5 Sherman Avenue, Suite 6
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Pred. No. 3
                                                              EKDPSTGKPLDPNTGLHPFDEDSGSL-----INP
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FILE REFERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 1721
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Best Local
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                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NELSON, RAPPLICANT: GUT, JIRI
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                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 94306-1840
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PatentIn Release #1.0, Version #1.30
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15 Sherman Avenue, Suite 6
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Pred. No. 8;
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PRIMATE INTRA-ACROSOMAL SPERM ANTIGEN TITLE OF INVENTION: FOR USE IN A CONTRACEPTIVE VACCINE NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                              APPLICANT: HERR, JOHN C.
APPLICANT: WRIGHT, RICHARD M.
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APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1238 -GDEIL-TEVLNITTDEVTGLPIDLETGLPRDPVSGLPQLPNGTLVDPSNK---KPIPGS 1292
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APPLICATION NUMBER: US/08/928,361B
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                                                                                                                                                        CITY: Arlington
STATE: Virginia
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                                                                                                                                      COUNTRY:
                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                   ADDRESSEE:
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1755 S. Jefferson Davis Highway, Suite 400
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Pred. No. 8;
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; TOPOLOGY: 11;
; MOLECULE TYPE:
US-08-292-045-5
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Patent No. 5824306
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Best Local S
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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APPLICANT: Blebm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 85
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/318,551
FILING DATE: 03-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                       SOFTWARE: WordPerfect for Windows, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GEHLSGEQSLG-EHASG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 AGNPRRNVTRSTVGRNVTLFDTTRMWAYRAVRHSWGGPV----AEWEHTVFEH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 ARVEQGLCDVLGGDASYGHRITKNPLSTAHATLWGPAD--ALYELRALAHTLDEIHALPE 167
                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: Windows 95
SOFTWARE: WordParfact f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 -IHLLNETIIADEFATG 232
                                                                                                                                                                                                                                 STREET: 1825 SHark
CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73
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CLASSIFICATION: 530
NIOR APPLICATION DATA:
                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                    ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 ARGTSGQSDESSG--SIDHQTSVQQLSGEFFSLENPSDAEALYETASGLNTLSE-HGSSE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Oblon, No. 5602005man REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 16-FEB-1990 APPLICATION NUMBER: US 0 FILING DATE: 27-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 285 amino acids
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                                                                                                                                                                                                                                                                E: Heska Corporation
1825 Sharp Point Drive
                                                                                                                                                                                                           USA
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(703) 413-2220
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                                                       US/09/031,485
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                                                                                            Version
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; MOLECULE TYPE: protein US-09-031-485-33
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Best Local Similarity
"-* hes 79; Conserva
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 33, Application US/08847429A Patent No. 5827692 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/847,429 FILING DATE: 24-APR-1997 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1745 amino aci
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                 CURRENT APPLICATION DATA:
                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                     TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, TITLE OF INVENTION: USES THEREOF NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
                                                                                                                                                                            ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
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                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- EQQETSKEGTFGCQTTHEKEKDDDGGSLKTTMKDSHVRQIFFDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLPSP-----SYVSMNRVTTTGHIVYALK---NPVCLTDAARRRPINLLARVEQGL 116
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Blehm, E. Sc
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                                                                                                                                                                                                                                      Carol Talkington Verser,
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US/08/847,429A
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Pred. No. 3
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Best Local
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                                                                                                                                            COUNTRY:
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US-08-847-429A-33
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Patent No. 6065577

GENERAL INFORMATION:

APPLICANT: Tang, Liang

APPLICANT: Blehm, E. Scot

APPLICANT: Blehm
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 33:
                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows,
CURRENT APPLICATION DATA:
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NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 RARQKAISLRGA----SKGGKEGGHKGGIASGASRRAHTRQQFLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Fort Collins
STATE: Colorado
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGPVAEWEHTV---FEHIHLLNETIIADEFATGPLGLNELKHLSRSISRWVWRNFTPETF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- EQQETSKEGTFGCQTTHEKEKDDDGGSLKTTMKDSHVRQIFFDG 1696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGPIVE-ERTITTYEDDVAVNEEEIVDKIV--PLNEEEQEKWDRMV-REVEMNF----- 1652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTRS-----TVGRNVTLFD-----
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    Application US/09065474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carol Talkington Verser, Heska Corporation
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22.8%; Pred. No. 3
US/09/065,474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-904-452-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08904452 Patent No. 6083742
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Best Local Similarity 22.8%;
Matches 79; Conservative 31
                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Randazzo,
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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INFORMATION FOR SEQ ID NO:
                                                                                             MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1745 amino aci
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                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1653 -- EQQETSKEGTFGCQTTHEKEKDDDGGSLKTTMKDSHVRQIFFDG 1696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1602 NGPIVE-ERTITTTYEDDVAVNEEEIVDKIV--PLNEEEQEKWDRWV-REVEMNF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1542 VTMAQQRLAQEPFFQQVGYNGTPGDPEEPKEQSFHEEEEEVAVSEIRTVVRTERHVHDSE 1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1504 AEKLDG-----LEGTPVS--HIS--GPS-----ITLSSTLLEV-----AGDRRRHAE 1541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1445 ALEVPDIDIRQVRHQLVGLEAVTILRIWIFLKKEQATPVALRSALQRIGRDDVVR-EMDR 1503
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REFERENCE/DOCKET NUMBER: HW-5-C1
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CLASSIFICATION:
                                            CLASSIFICATION:
                                                                  FILING DATE:
                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 94608-2916
                                                                                                                                                                                                                                                                              CITY: Emeryville
STATE: California
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 GLPSP-----SYVSMNRVTTTGHIVYALK---NPVCLTDAARRRPINLLARVEQGL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 ALELP-YIEANPLYMQSLVITDRDASD-----------ADWAADLA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                              31-JUL-1997
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                                                                                  US/08/904,452
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Pred. No. 3
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RESULT: 12
US-08-683-908-1
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 4:
TELEFAX: (212) 382-2124 INFORMATION FOR SEQ ID NO:
                                                                                                                            APPLICATION NUMBER: US/08/683,908
FILING DATE: 19-7UL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185626/1995
FILING DATE: 21-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                               SOFTWARE: MS-DOS Editor CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
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                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 768-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Shimizu, Sakayu
APPLICANT: Kobayashi, Michihiko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 HTLDEIHALPEAGNP----RRNVTRSTVGRNVTLFDTTRMWAYRAV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 RVEQGLCDVLGGDASYGHRITKNP------LSTAHATLWGPADALYELRALA 156
                                                                         NAME: Davidson, Clifford M
REGISTRATION NUMBER: 32,72:
REFERENCE/DOCKET NUMBER: 31
                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 ADLAGLESPSYVSMNRVT-----TTGHIVYALKNPVCL---TDAARRRPINLLA 110
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21.7%; Pred. No. 13;
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Expression of Nitrilase Gene,
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3ER: 3821004
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US-08-342-930-2
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Best Local S
Matches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08342930 Patent No. 5821084
                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1711 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION: APPLICANT: OLMSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                    REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Rel
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: I ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
LENGTH: 1/11
LENGTH: 1/11
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 RRNVTRSTVGRNVTLFDTTRMWAY-----RAVRHSWGGPVAEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 D--VLGGDASYGHRITKNPLSTAH----ATLWGPADALYELRALAHTLDEIHALPEAGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 ATDAGDLAEVASLHNSAVDLLSAAIRT----ELADQAAASDGLLE----CVLAYIRQNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 YDILFPTDWRMSVFQFPRYSFGFTED-----FIGRMTAVNVGGDRGIGRVVSSFMTSIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 DPNLCASQIAAEHNVS---VRTLHRLFSATGQGVAEHIRNLR-----LERIKT--ELADP
                                                                                     TELEFAX: (41)
                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/342,930 FILING DATE: 21-NOV-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: J1 CELL TYPE: unicellular organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 319 AMINO ACID RESIDUES
TYPE: AMINO ACID
TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASDADWAADLAGLPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLC
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: CA
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DAVIS, ALAN R.
DIXON, JACK E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                     (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MORRISON & FOERSTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.8%; Score 77; DB 2; Length 319; 21.3%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSTEOBLAST-TESTICULAR PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                           20344-20975.00
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                                                                                                                                                                                                                                                                                                     Version #1.30
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US-09-413-814-42
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                                                                                                                                                                                                                                                                           ; ORGANISM: Sorangium cellulosum US-09-413-814-42
                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 42
LENGTH: 2539
                                                                                                                                                                  Query Match
Best Local Similarity
Matches 42; Conserv
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dougherty, Brian APPLICANT: Goldberg, Steven APPLICANT: Hofle, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gesellschaft fuer Biotechnologische Forschung APPLICANT: Bristol-Myers Squibb, Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Beyer, Stefan
                                                                                                                                                                                                                                                                                                                    TYPE: PRT
1629 ALCIPQQYPHLETSHVDLGVVHADELHAARQLDSLLAECLSATAERQLALRGRHRWLLDY 1688
                                                                                 1586 HLVQA----
                                   780 SDAGHLS-----WE----QPLKLGQELFMLRDLTPG 806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            638 --TLWGSERSSSANATGWTPPSAPTLVNVTSDAPTQLQVSWAHVPGGRSRY--QVTLYQE 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580 AALKASWYHPPGGRDAFHLRLYRLRPLTLESEKVLPREAQNFSWAQLTAGCEFQVQLS-- 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 NELKHLSRSISRWVWRNFTPETFRARQKAISLRGASKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          720 YKVEVISWAGPLYTAAANVSAWTYPLIPNELLVSMQAGSAVVNLAWPSGPLGQGACHAQL 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 YRAVRHSWGGP-----VAEWEHTVFEHIHLLN----ETIIADEFATGPLG------L
                                                                                                         86 HIYYALKNPYCLTDAARRRPINLLARVEQGLCDYLGGDASYGHRITKNPLSTAHATLWGP 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 SAEKSGAYRHVTRQRALELPYIEANPLVMQSLVITDRDASDADWAADLAGLPSPSYVSMN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 4.8%; Score 77; DB 2; Length 1711; Local Similarity 20.1%; Pred. No. 42;
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                                                                                                                                                                    Conservative
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                                                                                   --MAEAGYSHPIRLLI-VSCGVYDVTGAE
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                                                                                                                                                               20; Mismatches
                                                                                                                                                                                     Score 77; DB 4; Length 2539; Pred. No. 78;
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                                                                                                                                                                  57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthesis of polyketide
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                                                                                                                                                                    Indels
                                                                                   -PLQPARATMIGP
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NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 3739
TYPE: PRT
ORGANISM: Streptomyces venezuelae
US-09-320-878-2
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CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER APPLICATION NUMBER: 60/10,880
EARLIER APPLICATION NUMBER: 60/087,080
EARLIER FILING DATE: 1998-09-28
EARLIER APPLICATION NUMBER: 60/087,080
EARLIER FILING DATE: 1998-05-28
EARLIER FILING DATE: 1998-05-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: McDANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1723 AEHLARTTS 1731
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                                                       680 AARV-----
                                                                                                                                                            624 APTLERVDVVQPVTFAVMVSLAKVWQHHGVTPQAVVGH----SQGEIAAAYVAGALTLDD 679
                                                                                                                                                                                                                                                                                                                                                                                529 AGGRAEFEHRAV--VLGT-----GODDFAQALTA------PEGLIRGTP----- 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       491 ------LVSAKTPAAL-DAQIGR---LAAFASQGRTDAADPGAVARVL 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         442 LRRAAVSSFGVSGTNAHVVLEEAPAAEETPASEATPAVEPSV-----GAGLVPW------ 490
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                                                                                                                                                                                                                                                                                                                                                                                                                               120 LGGDASYGHRITKNPLSTAHATLWGPADALYELRALAHTLDEIHALPEA----GNPRRNYT 176
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                                                                                                    239 LKHLSRSISRWVWRNFTPETFRARQKAISLRGASKGGKEGGHKGGIASGASRRAHTRQQF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 LPSPSYVSMNRVTTTGHIVYALKNPVCLTDAARRRPINLLARVEQGLCD------V 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 LPRKPLASAEKSGAYRHVTRQR---ALELPYIEANPLVMQSLVITDRDASDADWAADLAG 69
                                                                                                                                                                                                                      GPVAE-----
                                                                                                                                                                                                                                                                   -SDVGRVAFVFPGQGTQWAGMGAELLDVSKEFAAAMAECESALSRYVDWSLEAVVRQAPG 623
                                                                                                                                                                                                                                                                                                                           RSTVGR------NVTLFDTTRM-----
--LEGLS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 23; Mismatches 100; Indels 162; Gaps
                                                  -----VTLRSKSIAAHLAG-------KGGMISLALSEEATRQRI 715
                                                                                                                                                                                                                 ----WEH-----TVFEHIHLLNETIIADEFATGPLGLNE 238
                                                                                                                                                                                                                                                                                                                     -----WAYRA-VRHSWG 203
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Db 716 ENLHGLS 722

Search completed: October 4, 2002, 15:33:40 Job time: 32 sec



Run š

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Title:
Perfect score:
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Maximum DB
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     score greater than or equal
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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Listing first 45 summaries
     BLOSUM62
Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-08-94-907-20
PCT-US96-10986-10
US-08-494-907-16
PCT-US96-10986-16
US-08-16-15-37-3
US-08-96-16-33-3
US-08-96-16-33-3
US-09-011-434-1
US-09-413-814-3
US-09-413-814-3
US-09-413-814-3
US-09-451-688-6
US-08-245-688-10
US-08-355-2708-17
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ALIGNMENTS

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; TOPOLOGY: 1; MOLECULE TYPE: US-08-446-875-8
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/446,87
FILING DATE: July 12, 1995
CLASSIFICATION: 435
CRISTICATION DATA:
APPLICATION NUMBER: 08/102,385
FILING DATE: August 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REGISTRATION NUMBER: 29,421
                                                                                                                                         TELEPHONE: (310) 788-
TELEFAX: (310) 277-12
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Paulson, James C.
APPLICANT: Wen, Xiaohong
APPLICANT: Livingston, Brian Duane
APPLICANT: Gillespie, William
APPLICANT: Kelm, Sorge
APPLICANT: Burilingame, Alma L.
APPLICANT: Burilingame, Alma L.
APPLICANT: Medzihradszky, Katalin
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                         REGISTRATION NUMBER: 29,421
REFERENCE,DOCKET NUMBER: 111-197
TELECOMMUNICATION INFORMATION:
                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
                                                               TYPE: amino acid
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                                                                                   375 amino acids
                                             linear
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10) 277-1297
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                                                                                                                        Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                         Matches
                                                                                                                                                                                                                                                                             TELEFAX: (310) 277-1297 INFORMATION FOR SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 04-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 04-AUG-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925369
FILING DATE: 04-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Identification and Synthesis of Sialyltransferases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1:0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 KQILKFLNAEKNISVLKGTLKPGNIIHYIFNRNST 132
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                57
                                            52 SNRAEVVINGSSLPAVANRSNESLKHSIQPASSKW----
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                                                                                                                                                                                                                                              LENGTH:
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                                                                         2 TTRERLPRNGYSIAAAAKKLGVS-----ESTVKRWTSEPREEFVARVAARHARIRELRSE 56
GQSMRAIAAEVGVSV--GT-----VHYALNKNRT 83
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Gillespie, William
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                                                                                                                                                                                                                                                                                                             (310)788-5000
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25.3%;
                                                                                                                      16.1%; Score 67.5; DB 2; Length 375; 25.3%; Pred. No. 0.75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/102,385G
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                                                                                                                                                      US-08-494-907-20
                                                                                                                                                                     RESULT
                                                                                                      Sequence 20, Applicat Patent No. 5955298 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Apparent No. 597
                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 amino acids
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICANT: Weller, Davis...
APPLICANT: Cook, R. James
TITLE OF INVENTION: Sequences for Production of
TITLE OF INVENTION: 2,4-Diacetylphloroglucinol and Methods
TITLE OF SERGIENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HUMAN HYDROXYPYRUVATE REDUCTASE NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                 APPLICANT: Thomashow, Linda S APPLICANT: Bangera, Mahalaxmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hillman, Jennifer APPLICANT: Lal, Preeti APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                              54 RSEGQSMRAIAAEVGVSVGTVHYALNK 80 : | ::: |: : :|| | | | ||::
                                                                                                                                                                                                                                                                                                                                                                                                                                             14 RIPAEGRVALARA-----ADCEVEQWDSDEPIPAKELERGVAGAHGLLCLLSDHVDKRIL 68
                                                                                                                                                                                                                                                                                                                                                       DAAGANLKVIST---MSVGIDHLALDE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLPRNGYSIAAAAKKLGVSESTVKRWTSE---PREEFVARVAARHARI-----
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                                                                                                                                                                                                                                         Application US/08494907
                                                                                                                       Bangera, Mahalaxmi
Weller, David M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.8%; Score 62; 26.4%; Pred. No.
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PCT-US96-10986-20
Sequence 20, Application PC/TUS9610986; GENERAL INFORMATION:
TITLE OF INVENTION: Sequences for 1
TITLE OF INVENTION: 2,4-Diacetylph
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Best Local Similarity 21.9%;
Matches 21; Conservative 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMMUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Pendorf, Stephan A.
REGISTRATION UMBER: 32665
REFERENCE/DOCKET NUMBER: A7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Stephan A. Pendorf, DOMINIK & STEIN
STREET: 600 N. West Shore Boulevard, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acid
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NAME: Connor, Margaret A
REGISTRATION NUMBER: 3004
REFERENCE/DOCKET NUMBER:
                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STREET: ...
Tampa
                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                     COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 NLNFLLLNLWKVWRETICGEAFRCVIAEAQLDPSTL 123
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Pred. No. 1.1;
L1; Mismatches 25; Indels 3
                     A700.320
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US-08-494-907-16
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 Matches
                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16,
                                                                                                                                                       TELEFAX: (510) 559-577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (813) 289-2966
TELEFAX: (813)289-2967
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Thomas
APPLICANT: Banger
APPLICANT: Weller
APPLICANT: Cook,
                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Sequences for Production of TITLE OF INVENTION: 2,4-Diacetylphloroglucinol and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 800 B
CITY: Albany
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                      TELEPHONE: (510)
                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                LENGTH: 202 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                               NAME: Connor, Margaret A REGISTRATION NUMBER: 300
                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UZIP: 94710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 NLNFLLLNLWKVWRETICGEAFRCVIAEAQLDPSTL 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 130 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08494907
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   Conservative
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Weller, David M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomashow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Margaret A. Connor, USDA-ARS
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                  14.6%;
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                                                                                                                                                                                                                                                               30043
; Score 61.5; I; Pred. No. 2; 11; Mismatches
                                                                                                                                                                                                                                               0009.95
                              DB 2;
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   25;
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                                Length 202;
 Indels
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   39;
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Gaps
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US-08-160-524A-12
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PCT-US96-10986-16
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; MOLECULE TYPE:
PCT-US96-10986-16
                                                                                                                                                                 Sequence 12, Application US/08160524A Patent No. 5851761
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (813)289-296 INFORMATION FOR SEQ ID NO:
                                                                        APPLICANT:
APPLICANT:
                  TITLE OF INVENTION: PROBES, KITS AND METHODS FOR THE TITLE OF INVENTION: DETECTION AND DIFFERENTIATION OF MYOCBACTERIA NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephan A. Pendorf, DOMINIK & STEIN
 CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                           APPLICANT:
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STATE: FL
                                                                                                                                                                                                                                                                                                                 57
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(813)289-2967
                                                                      Catty, David
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                                                                                       Dale, Jeremy W.
Zainuddin, Zain
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                                                                                                                           McAdam, Ruth Anne
                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                             -----GOSMRAIAAEVGVSVGTV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                          14.68;
21.98;
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                                                                                         Zainul Fadziruddin B.
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Pred. No. 2;
L1; Mismatches
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US-08-473-020A-26
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                                                                                                                                                                                                                    Patent No.
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                                                                                                                                                                                                                    Sequence 26, Application US/08473020A Patent No. 5877273
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                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                         APPLICANT:
                                                                                     APPLICANT: Gicquel, Brigitte TITLE OF INVENTION: Nucleotic TITLE OF INVENTION: applicat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/08/160,524A
FILING DATE: 01-DEC-1993
                 NUMBER OF SEQUENCES: 3
                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: GB 91 FILING DATE: 09-JAN-1990 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: GB 8:
FILING DATE: 22-FEB-1989
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                60 MRAIAAEVGVSVGTVHYA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/GB90/00276 FILING DATE: 22-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 4 Embarcades
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                            80 ERDI-----LKKATAYFA 92
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      7 LPRNGYSIAAAAKKLGVSESTVKRWTS-----EPREEFVARVAARHARIRELRSEGOS 59
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94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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E: Attn: Walter H. Dreger
4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 amino acids
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                                                                                                                                                                                Allan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.5%; Score 61; DB 2
23.1%; Pred. No. 0.88;
                                  application as 31
                                                                  applications to the synthesis or detection of nucleic acids, products of expression of such sequences and
                                                                                                        Nucleotide sequences of actinomycetales,
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FILING DATE:

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US-08-491-357-3
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FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H
REGISTRATION NUMBER: 24190
REFERENCE/DOCKET NUMBER: A54435
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
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INFORMATION FOR SEQ ID NO:
                ZIP: 19103-2307

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    APPLICANT: Law, Susan
APPLICANT: Estojak, Joanne
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING A SIGNAL
TITLE OF INVENTION: MEDIATOR PROTEIN THAT INDUCES CELLULAR MORPHOLOGICAL
TITLE OF INVENTION: ALTERATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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TYPE: amino acid
STRANDEDNESS: single
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CITY: San Francisco
                                                                                                                                                             COUNTRY:
APPLICATION NUMBER:
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1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 Embarcadero Center, Suite 3400
                                                                                                                                                             USA
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US/08/491,357
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                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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GENERAL INFORMATION:
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Best Local Similarity 34.5
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Golemis, Erica A.
APPLICANT: Law, Susan
APPLICANT: Estojak, Joanne
TITLE OF INVENTION: MUCLEIC ACID MOLECULE ENCODING A SIGNAL
TITLE OF INVENTION: MEDIATOR PROTEIN THAT INDUCES CELLULAR MORPHOLOGICAL
TITLE OF INVENTION: ALTERATIONS
                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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LENGTH: 872 amino acids
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dann, Dor
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                                                         LENGTH:
TYPE: a
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          TYPE: amino acid
STRANDEDNESS: No. 6100384 Relevant
TOPOLOGY: No. 6100384 Relevant
                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                          872 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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protein
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                                                                                                                                                                                                                                                                                      US/08/491,357
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US-08-968-633-3
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US-09-196-466-3
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GENERAL INFORMATION:
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Best Local Similarity 34.5
Matches 19; Conservative
                                                            Matches
                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
ZIP: 19103-230,
ZIP: 19103-230,
COMPUTER READABLE FORM:
COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: PC-DOS/MS-DOS
Palease #1.0,
                                                                                                                                                                                                                                                                                      TELEFAX: (215) 563-40 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
                                                                                                                                                                        MOLECULE TYPE: pi
                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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APPLICANT:
                                                                                                                                                          ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           493 RSTSEPQEPPVQDLKAAVAAVHGAVHELLEFARS--AVSSATHTSDRTLHAKLSR 545
493 RSTSEPQEPPVQDLKAAVAAVHGAVHELLEFARS--AVSSATHTSDRTLHAKLSR 545
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CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 RWTSEPRE----EFVARVAARHARIRELRSEGQSWRAIAAEVGVSVGTVHYALNK 80
                            30 RWTSEPRE----EFVARVAARHARIRELRSEGQSMRAIAAEVGVSVGTVHYALNK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                      TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Golemis, Erica A.
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                                                              Conservative
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                                                                                                                                                                                                                                                                               5) 50
563-4044
3: NO: 3:
                                                                                                                                                                                                                         not relevant
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                                                           14.3%; Score 60; DB 34.5%; Pred. No. 23; tive 10; Mismatches
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Pred. No. 23;
10; Mismatches
                                                                             DB 3;
23;
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                                                                                        Length 872;
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                                                            Indels
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RESULT

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RESULT 14
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                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09071434
                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Sven, H
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION UNMER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 872 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US96/10823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ESTOJAK, JOANNE TITLE OF INVENTION: MUCLEIC TITLE OF INVENTION: MEDIATI TITLE OF INVENTION: ALTERAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Golemis, Erica A. APPLICANT: Law, Susan APPLICANT: Estojak, Joanne
                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                            APPLICANT: COTÎCY, NCÎL C.
APPLICANT: BAUGHN, MATÎCH
TITLE OF INVENTION: HUMAN BRAÎN-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                         493 RSTSEPQEPPVQDLKAAVAAVHGAVHELLEFARS--AVSSATHTSDRTLHAKLSR 545
                                COUNTRY:
                                                     CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                          30 RWTSEPRE----EFVARVAARHARIRELRSEGQSMRAIAAEVGVSVGTVHYALNK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 34.5
nes 19; Conservative
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CLASSIFICATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 19103-2307
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                                                                                         STREET:
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                                                                                                          ADDRESSEE:
                    94304
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                                                                                         3174 Porter Dr.
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                                      USA
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                                                                                                            Incyte Pharmaceuticals, Inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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SOFTWARE: FastSEQ for I

FastSEQ for Windows Version 2.0

US/09/071,434

APPLICATION NUMBER: US/09/0: FILING DATE: Filed Herewith

OPERATING SYSTEM: DOS

MEDIUM TYPE:

Diskette

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US-08-335-844A-22
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Best Local Similarity 31.9%;
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                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 APPLICANT: SMITH, TREVOR STANLEY
APPLICANT: MUNN, EDWARD ALBERT
APPLICANT: KNOX, DAVID PATRICK
APPLICANT: OLIVER, JOANNA JANE
APPLICANT: NEWTON, SUSAN ELIZABETH
APPLICANT: NEWTON, SUSAN ELIZABETH
TITLE OF INVENTION: RECOMBINANT DNA MOLECULES ENCODING
TITLE OF INVENTION: AMINOPEPPIDASE ENZYMES AND THEIR USE IN THE PREPARATION OF
TITLE OF INVENTION: VACCINES AGAINST HELMINTH INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: BRAIN
CLONE: 662575
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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                                                                                                                                                                                                 CITY: Washington STATE: D. C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lin
APPLICATION NUMBER: US/0 FILING DATE: 09-JAN-1995
                                                                                                                                                               ZIP:
                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                               20004
                                                                                                                                                                                U.S.A.
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              US/08/335,844A
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                                                                    Matches
                                                                                 Query Match 13.8%;
Best Local Similarity 28.1%;
                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: GB PORTION DATE: 06-MAY-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 977 amino acids
                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 35,400
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: GB 9: FILING DATE: 08-MAY-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                     MOLECULE TYPE: protein
                24 SESTVKRWTSEPREEFVARVAARHARIRELRSEGQSMRAIAAEVGVSVGTVHYALNK 80 : : : : | : | : | : | : | |
                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                          TELEPHONE:
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3 AEESQEQETQQPRKNTVLRLTP----IKSL----FALLVVAAAVGLSIGLTYYFTRK 51
                                                                    16;
                                                                                                                                                                                                                                                                                                                                      WALKER, Barbara W.
WALKER, Barbara W.
11
                                                                                                                                                                                                                                                                       (202)783-6031
                                                                  Conservative
                                                                                                                                                                                                                                                                                          (202)783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                 GB 9209936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB PCT/GB93/00943
                                                                14;
                                                                                 Score 58; DB Pred. No. 50;
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                                                                  Mismatches
                                                                                                 DB 3; Length 977;
                                                                19; Indels
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Gaps

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Search completed: October 4, 2002, 15:33:41 Job time: 33 sec

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Result
No.
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Maximum DB
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Maximum Match 100
Listing first 45
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                         Score
                                                                                 96
82.5
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_inverteb:
5: sp_macmal:*
7: sp_mhc:*
8: sp_organel:
9: sp_phage:*
10: sp_plant:*
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length: 2000000000
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Match
   100.0
381.2
38.3
33.3
228.8
226.2
226.2
119.5
118.6
118.6
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118.6
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Gapop 10.0 , Gapext 0.5
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046076 corynebacte
09f4v5 brevlbacter
09f1y5 rhodococcus
09f5n5 rhodococcus
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031456 propionibac
04527 bifidobacter
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O1-MAR-2001 (TrEMBLrel. 1
O1-MAR-2001 (TrEMBLrel. 1
O1-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jore J.P.M., van Luijk N., Luiten R.G.M., van der Werf M.J., Pouwels P.H.;
"Efficient transformation system for Propionibacterium freud based on a novel vector.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21091935; PubMed=11157209;
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NCBI_TaxID=1744;
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Q46076;
01-NOV-1996
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases EMBL; AY004211; AAF89086.1; ...
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"Complete Nucleotide Sequence of a Plasmid pXZ10142 from
Corynebacterium glutamicum.";
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; X72691, CAA51239.1; ...
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
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Pred. No. 1.3e-14;
7; Mismatches 18
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Q9LBJ5;
Q1-OCT-2000
01-OCT-2000
01-DEC-2001
DNA-BINDING
                                                                                                                                                                 DNA-binding; FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB040101; BAA92819.1; -.
InterPro; IPR000792; HTH_LuxR.
DNA-binding; Plasmid.
SEQUENCE 93 AA; 10124 vm
                                                                                                                                                                                                              Ryabchenko L.E., Novikov A.D., Golyshin P.N., Yanenko A.S. "Rhodococcus erythropolis plasmid pN30 putative replicase putative DNA-binding replication protein (ORF2)."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF312210; AAG29855.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9F5N5;
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MEDLINB-21196497; PubMed-11302154;
Hirasawa K., Ishii Y., Kobayashi M., Koizumi K., Maruhashi K.;
"Improvement of Deulfurization activity in Rhodococcus erythropolis
KA2-5-1 by Genetic Engineering.";
Biosci. Biotechnol. Biochem. 65:239-246(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
putative DNA-BINDING PROTEIN.
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    RNGYSIAAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELRSEGQSMRAIAAEVG
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31; Conserv
                                              Similarity 37.8
28; Conservative
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                                                                                                                                                                      10409 MW;
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Pred. No. 5.7e-07;
4; Mismatches 23;
                                                 Score 121; DB 2;
Pred. No. 4.9e-05;
4; Mismatches 32;
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Best Local S
Matches 25
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"Structural analysis of the 6-kb cr Rhodococcus erythropolis NIB6/21 an Rhodococcus shuttle vectors.";
Microbiology 143:3137-3147(1997).
EMBL; AF015088; AAC45811.1;
DNA-binding; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000
01-OCT-2000
01-MAR-2001
                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Propionibacterineae; Propionibacterium.

NCBI_TaxID=1749, 1748;
[1]
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                                                                     SPECIES-P.jensenii; STRAIN-DFI;
Stierli M.P., Meile L., Teuber
"Molecular analysis of plasmid
Propionibacterium jensenii.";
                                                                                                                                                                                                                                                                                                      Propionibacterium jensenii, and Propionibacterium acidipropionici Propionibacterium acidipropionici Plasmid pLMEIO6, and Plasmid pRGO
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STRAIN=N186/21;
MEDLINE=98015402; PubMed=9353918;
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Plasmid prAJZ600.
Bacteria; Firmicuttes; Actinobacteria;
Actinomycetales; Corynebacterineae; Nc
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(TrembLrel. 15, Last sequence update)
(TrembLrel. 16, Last annotation update)
L 13.0 KDA PROTEIN (REPLICATION PROTEIN)
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llarity 35.7%;
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  N.A.
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                                                                                                                                         STRAIN-DF1; PLASMID-PLME106;
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                                               EMBL/GenBank/DDBJ databases
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Pred. No. 0.00063;
2; Mismatches 33;
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Propionibacteriaceae;
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                          Q52144;
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Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
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Q45287;
01-NOV-1996
01-NOV-1996
01-DEC-2001
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EMBL; X84655; CAA59149.1;

SEQUENCE 105 AA; 12317 MW; 295DD1583018
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EMBL; AJ250233; CABB8397.1; -.
EMBL; AB007909; BAB17920.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 114 AA; 13048 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=B2577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORF1 PROTEIN.
   HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96341130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bifidobacterium longum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kiatpapan P., Hashimoto Y., Nakamura
Yamashita M., Murooka Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=P.acidipropionici; STRAIN=E214; PLASMID=PRGO1; MEDLINE=20509786; PubMed=11055911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-1679;
                                                                                                                                                                                                                                                                                                                                                                                      61 RAIAAEVGVSVGTVH---YALNKNRTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 TSRHFGIAKTTAQERARRARRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                            62
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                                                                                                                                                                                                                                                                                                                         PQTAEHFNMSQGAVRQRCYRARKERED
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(TIEMBLIE1. 01, Created)
(TIEMBLIE1. 01, Last sequence update)
(TIEMBLIE1. 19, Last annotation updat, 13.7 KDA PROTEIN.
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                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.6%;
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19,
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Pred. No. 0.44
13; Mismatches
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Last annotation update)
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Bl from Bifidobacterium longum
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; Bifidobacterium.
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0.021;
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RESULT OPEXOS ID OF OCC. F. CO.
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Best Local :
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Q93Q22;
Q1-DEC-2001
01-DEC-2001
01-DEC-2001
                                               Q9EXO3 PRELIMINARY; PRT; 132 AA.
Q9EXO3; O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL (TrEMBLRE)
SECG38.16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M23557; AAA98172.1; -. Hypothetical protein; Plasmi SEQUENCE 119 AA; 13683 MW
                                                                                                                                                                                                                                                                                          "Yuen K.Y., Woo P.C.Y., Leung P.K.L.;
"Insertion sequence of Burkholderia pseudomallei.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF287534; AAK58883.1;
-.
SEQUENCE 87 AA; 10211 MW; 69505094D5308D0E CRC64;
  Actinomycetales; Streptomycineae; NCBI_TaxID=1902;
                         Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                  Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria; Proteobacteria; beta subdivision; Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSPOSASE A.
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Rauzier J., Moniz-Pereira J., Gicquel-Sanzey
"Complete nucleotide sequence of pAL5000, a p
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NCBI_TaxID=1766;
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Plasmid pAL5000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELR-SEGQSMRAIAAEVGVSVGT 73
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                                                                                                                                                                                                                                  19; Conserv
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nilarity 36.1%;
Conservative
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119 AA; 13683 MW;
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                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 82; DB:
Pred. No. 0.57;
8; Mismatches
                                                                                                                                                                                                                                 Score 79; DB Pred. No. 0.81 9; Mismatches
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             Streptomycetaceae;
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Query Match Best Local

Similarity

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Score 78; DB 1 Pred. No. 1.9; 17; Mismatches

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Best Local 9
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She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G., Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A., De Moors A., Erauso G., Fletcher C., Gordon P.M.K., Heikamp de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N. Charlebois R.L., Doolittle W.F., Dupuet M., Gaasterland T., Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.; "The complete genome of the crenarchaeon Sulfolobus solfataricus Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

EMBL; AE006677; AAK40779.1; -
Hypothetical protein; Complete proteome.

ESQUENCE 150 AA; 17577 MW; E14E9250440E56B6 CRC64;
                                                                                                                                                                                                                                                                                                                        Q97ZW9;
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Saunders D.C., Harris
Submitted (OCT-2000)
                                                                                                                                                                                                                 Sulfolobus solfataricus Archaea; Crenarchaeota; NCBI_TaxID=2287;
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Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed
                                                                                                                                                              STRAIN=ATCC 35092 / DSM 1617 / P2;
MEDLINE=21332296; PubMed=11427726;
                                                                                                                                                                                                                                                          SS00454.
                                                                                                                                                                                                                                                                     HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the 8 Mb Streptomyces coelicolor A3(2) Mol. Microbiol. 21:77-96(1996). EMBL; AL445503; CAC13075.1;
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Cerdeno A.M.,
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EQUENCE 132 AA; 1
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e EMBL/GenBank/DDBJ databases
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Last annotation update)
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Pred. No. 1.6;
9; Mismatches
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                                                        solfataricus P2.";
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Matches 29
Q9RJU2;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 17, Last annotation update)
TRANSPOSASE.
SC6A9. 26 OR SCJ11.20.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                           Submitted (AUG-1999) to the EMEL; AL031035; CAAL9911.1; --
EMBL; AL1091949; CAB52905.1; --
InterPro; IPRO01584; Rve.
Pfam; PF00665; rve; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              the 8 Mb Streptomyces coelicolo Mol. Microbiol. 21:77-96(1996).
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NCBI_TaxID=1902;
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(JUL-1998) to
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e EMBL/GenBank/DDBJ databases.
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Pred. No. 4.4;
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             PRT;
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TRANSPOSASE (PUTATIVE IN:
SCF41.27 OR SC10B8A.13
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Pfam; PF00665; r
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"A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacterida
Bacteria; Firmicutes; Actinobacteria; Actinobacterida
                        Actinomycetales;
NCBI_TaxID=1902;
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                                                                                   Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Submitted (SEP-1999) 1
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Redenbach M., Kieser H.M., Denapaite
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SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001584; Rve.
                                                                                                                                                                     (TrEMBLrel. 12, (TrEMBLrel. 12, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TIEMBLrel. 13, Created)
(TIEMBLrel. 13, Last sequence update)
(TIEMBLrel. 17, Last annotation update)
(PUTATIVE INSERTION ELEMENT TRANSPOSASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harris
                                                                                                                                                                                                                                                               PRELIMINARY;
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F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rve;
                                                               Streptomycineae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36544 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.6%;
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EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barrell B.G., Rajandream M.A
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 78; DB:
Pred. No. 4.4;
11; Mismatches
                                                                                                                                                                     Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
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                                                          Streptomycetaceae;
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                                                                                                                                                                                                                                                             338
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                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                          Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36
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OM protein - protein search, using sw model
                                                                                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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Sequence:	Perfect score:	Title:
1 MTTRERLPRNGYSIAAAAKK	420	US-09-720-583A-3

Run

October 4,

2002, 15:34:40 ;

Search time 55.08 Seconds (without alignments) 171.410 Million cell updates/sec

....EVGVSVGTVHYALNKNRTDA 85

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched 747574 segs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB Maximum DB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s summaries

Database 1: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
8: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*
9: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
10: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
12: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
16: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1995.DAT:*
18: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*
20: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1996.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
23: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
24: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
25: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
26: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
27: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
28: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
29: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
20: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match Length DB	ength	DB	ID	Description
1	420	100.0	85	21	AAY44637	Propionibacterium
2	82	19.5	314	18	AAW14834	Protein encoded by
ω	.79	18.8	314	13	AAR29623	Tet e gene product
4	79	18.8	314	13	AAR37873	Tet e gene product
տ	79	18.8	314	14	AAR34544	Tet e gene product
6	76	18.1	314	13	AAR20991	Protein "d" encode
7	69.5	16.5	316	21	AAB14150	Bordetella pertuss
8	67	16.0	98	22	AAG91658	C glutamicum prote
9	67	16.0	279	22	AAU44478	Propionibacterium
10	67	16.0	927	22	AAE10133	Streptomyces nours
11	66	15.7	214	22	AAU59374	Propionibacterium

4.4	A (.	2	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
62	n 6	62	62	62	62	62	62.5	63	63	63	63	63		63.5				63.5				•	•	•				64	64	64	65	65.5
14.8	14.8		•	•	•	•	•	•	•	•	•	•	•	15.1	15.1	15.1	15.1	15.1	15.1	15.1	15.1	15.1	•	15.1	15.1		•	٠	•	•	15.5	•
362	328	328	227	204	186	158	507	2169	284	279	247	219	953	763	580	573	547	326	211	186	186	186	186	186	186	98	98	1100	743	162	868	132
22	3 N	20	21	21	21	21	22	22	21	<u>2</u> 2	21	22	21	21	21	21	22	22	22	19	19	19	19	19	18	22	22	22	22	22	22	22
AAU22915	AAB42600	AAY43622	AAG40789	AAG40790	AAG40791	AAY81764	AAB96433	AAG91701	AAG20357	AAG20358	AAG20359	AAU63583	AAY82156	AAY82155	AAY82157	AAY82154	AA013897	AAU34593	AAU52836	AAW44287	AAW44286	AAW44289	AAW44288	AAW50189	AAW30754	AAG90753		ABG24905	ABB68417	AAU56724	ABB64106	AAU58347
Novel human enzyme Novel human enzyme	ORFX	hydroxypy	mays protein	Zea mays protein f	Zea mays protein f	Streptococcus pneu	Putative P. abyssi	3			Arabidopsis thalia	ä				Pseudomonas putida	ര	E. coli cellular p	terium	coli		coli	Escherichia coli D	0	E. coli Cam operon	C glutamicum prote	C glutamicum prote	Novel human diagno	Drosophila melanog	Propionibacterium	Drosophila melanog	Propionibacterium

ALIGNMENTS

7

AAY44637 ID AAY4 RESULT _

AAY44637 standard; Protein; 85 ₿

AAY44637;

07-APR-2000 (first entry)

Propionibacterium LMG 16545 protein-2.

Propionibacterium LMG 16545; vector; plasmid; antigen; vaccine; nutritional factor; growth factor; clotting factor; antimicrobia hormone; vitamin B12; animal feed; lactic acid bacteria; foodstu

Propionibacterium freudenreichii LMG 16545

W09967356-A2

29-DEC-1999

25-JUN-1999; 99WO-EP04416

25-JUN-1998; 98EP-0305033

(KONN) GIST-BROCADES BV.

Pouwels PH, Van Luijk N, Jore JPM, Luiten RGM;

WPI; 2000-136977/12. N-PSDB; AAZ49691.

Novel vectors containing Propionibacterium sequences, used to homologous or heterologous proteins ${\ \ }$ express

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present amino acid sequence is encoded by the endogenous plasmid Propionibacterium LMG 16345 ORR-2, derived from Propionibacterium freudenreichil deposited under CBS 101022 or CBS 101023. The vector has insertion sites for foreign DNA fragments and is capable of autonomous replication. It can be used safely as they remain extrachromosomal and are very stable. They can be used to express homologous or heterologous proteins, which may include antigens for use in vaccines, nutritional, growth and clotting factors, antimicrobials, vitamins (especially vitamin B12), enzymes, hormones and drugs. The Propionibacterium host cells are used in the production of animal feeds, manufacture of foodstuffs like, sausages and cheese, where they may be used instead of or in addition to lactic acid bacteria and in the manufacture of vitamin B12. The DNA sequence can also be used as a source of primers and probes.
                                                                 Mycobacteria expressing secretion signal of lipoprotein and heterologous antigen, esp. outer surface protein A or B of Borrelia burgdorferi - are used in the form of a live bacterial vaccines
                                                                                                                                                                        Stover
                                                                                                                                                                                                                                                                                                                                                                                     surface protein.
                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pMV101; Mycobacteria; lipoprotein antigen; bacterial vaccine; Lyme disease;
                          Example 1;
                                                                                                                                          WPI; 1997-042315/04.
                                                                                                                                                                                                                               17-NOV-1992;
21-OCT-1991;
                                                                                                                                                                                                                                                                        21-OCT-1991;
                                                                                                                                                                                                                                                                                                    10-DEC-1996
                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein encoded by M.rep ORF1 of plasmid pMV101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW14834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW14834 standard; Protein; 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                            N-PSDB; AAT64413.
                                                                                                                                                                                                  (MEDI-) MEDIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 16; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                         Fig
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                                                       disease
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P
                         5; 122pp; English.
                                                                                                                                                                                                                             92US-0977630.
91US-0780261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; 54pp; English.
                                                                                                                                                                                                                                                                        91US-0780261.
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Pred. No. 3.2e-46;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                    secretion signal sequence;
Borrelia burgdorferi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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The sequences

given in AAW14834-36 are

proteins which

are encoded

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Query Match

18.8%;

Score

79; DΒ

13;

Length 314;

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RESULT
AAR29623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the plasmid pMV101. This plasmid was used in the construction of series of vectors used to produce the recombinant Mycobacteria of the invention. The recombinant mycobacteria of the invention are transformed with DNA encoding a polypeptide which comprises a lipoprotein secretion signal sequence and an antigen (Ag) heterolo to the mycobacteria. The lipoprotein secretion signal causes the to be produced as a lipoprotein. The mycobacteria may be used in form of a live bacterial vaccines against Lyme disease, where the bacteriae express a surface protein of Borrelia burgdorferi, the causative agent of Lyme disease. This sequence is printed in the specification in the C-terminal to N-terminal orientation as
                                                                                                                                                                                                                                                                                                                                                                                               cytotoxic T-lymphocyte response; transformed Mycobacteria; BCG; Mycobacterium smegmatis; vaccine; cell mediated immunity; HIV; pertussis; malaria; influenza virus; CTL; herpes virus.
Sequence
                            This sequence is the
                                                                                              Method of inducing cytotoxic T-lymphocyte response - esp. expression products of transformed Mycobacterium are useful as vaccines against HIV, pertussis, malaria, influenza virus, herpes
                                                                                                                                                                                                                                                          06-JUN-1991;
                                                                                                                                                                                                                                                                                                                                           W09221376-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tet e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR29623 standard; Protein; 314 AA
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                                                                                                                                                                                                  Dela Cruz V,
                                                                                                                                                                                                                              (MEDI-) MEDIMMUNE INC.
                                                                                                                                                                                                                                                                                      01-JUN-1992;
                                                                                                                                                                                                                                                                                                                 10-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium
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                                                                                                                                                         1992-433380/52.
DB; AAQ31727.
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                                                        ۳,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                        Fig
 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                          product from pMV101 - a deletion mutant of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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 æ
                                                      5; 86pp; English.
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                             tet e
                          gene encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 82; DB 18
Pred. No. 0.04;
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                            plasmid
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                            PMV101
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RESULT
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AC AAR3
AC AAR3
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XX
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AAR37873
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Best Local S
Matches 26
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Matches 26; Conservative
                             04-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytotoxic T-lymphocyte response; transformed Mycobacteria; BCG; Mycobacterium smegmatis; vaccine; cell mediated immunity; HIV; pertussis; malaria; influenza virus; CTL; herpes virus.
                                                                           AAR34544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dela Cruz V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-JUN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR37873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR37873 standard;
                                                                                                                  AAR34544 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the tet e gene encoded by plasmid pMV101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 5; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetanus vaccination - by provoking an immune response using transformed Mycobacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-433378/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tet e gene product from pMV101 - a deletion mutant of pYUB125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MEDI-) MEDIMMUNE INC
                                                                                                                                                                                                                             283
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                                                                                                                                                                                                                             vkrlgyrarker
                                                                                                                                                                                                                                                                       VH---YALNKNR 82
                                                                                                                                                                                                                                                                                                              aegaritglserhvvrlvaqersenlaeqaarrerirayeddegeswpqtakmfgleldt 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vkrlgyrarker 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aegaritglserhvvrlvaqersenlaeqaarrerirayeddegeswpqtakmfgleldt 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELR-SEGQSMRAIAAEVGVSVGT 73
                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stover CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-0711084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92WO-US05023
                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 314
                                                                                                                                                                                                                                                                                                                                                                                                                         18.8%;
                                                                                                                    314
                                                                                                                                                                                                                                                                                                                                                                                                     8;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 79;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.098;
8; Mismatches 34;
                                                                                                                    Ā
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                         0.098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                       34;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Best Local :
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                         09-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the tet e gene product encoded by plasmid pMY101. When the nucleotide was decoded, the sequence in the specification was found to contain several deletions and insertions which upset the reading frame. Also many codons were found to encode amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytotoxic T-lymphocyte response; transformed Mycobacteria; Mycobacterium smegmatis; vaccine; cell mediated immunity; pertussis; malaria; influenza virus; CTL; herpes virus.
                                                                                                             W09201783-A
                                                                                                                                                         Synthetic.
                                                                                                                                                                                                  Polymerase resistance;
                                                                                                                                                                                                                                                                  Protein "d"
                                                                                                                                                                                                                                                                                                              03-JUN-1992
                                                                                                                                                                                                                                                                                                                                                         AAR20991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-152187/18.
N-PSDB; AAQ41316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stover CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium
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                                                                    06-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                  AAR20991 standard; Protein; 314 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acids contrary to the universal genetic code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 5; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion protein of lipoprotein heterologous to bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-OCT-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                           chain reaction; mycobacterial promoter; kanamycin;
; BCG; Bacille Calmette-Guerin; origin of replicati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 AA;
                                                                                                                                                                                                                                                                  encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                           (first entry)
                         91WO-US04833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.8%;
                                                                                                                                                                                                                                                                  by mycobacterial plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 79; DB 14
Pred. No. 0.098;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14;
                                                                                                                                                                                                                                                                  DMV101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmid pYUB12 was constructed by ligating a 5kb Sau3 fragment from pAL5000 (contg. a replication origin from M.fortuitum) to BamHI-dispeted pIJ666 (contg. an E.coli ori and kanamycin-neomycin resistance sequences). A 2566bp HpaI-EcoRV fragment from pYUB12 (comprising the minimum sequence necessary for plasmid replication in BCG) was ligated to PYUBI-dispeted pYUB8 to form pYUB53. (Plasmid PYUB8 is a pBR322 deriv. which includes an E.coli replicon and a kanamycin resistance gene). Twelve restriction sites were removed by digesting pYUB53 with Aatl, EcoRV and PstI. To eliminate 792 bases of the (inactivated) tet gene, the plasmid was digested with Circularised. The resulting plasmid was designated pWT01. The nucleotide sequence of plasmid pWT01 is printed in the specification but the copy quality is too poor to allow the sequence to be included on the GENESEO nucleotide database. Three proteins are encoded by pMV101, i.e. the kanamycin resistance protein and proteins "d" and "e" encoded by the complementary strand. See also AAR20992 and AAR20993.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA site-specific integration into Mycobacteria - useful as adjuvant in vaccines and as therapeutic agent for malaria, influenza, herpes and human immunodeficiency virus
(ULBR ) UNIV
                                21-DEC-1998;
                                                                21-DEC-1999;
                                                                                                29-JUN-2000
                                                                                                                                WO200037493-A2
                                                                                                                                                            Bordetella pertussis
                                                                                                                                                                                           Type III secretion system; virulence
                                                                                                                                                                                                                           Bordetella pertussis protein # 4.
                                                                                                                                                                                                                                                              02-FEB-2001
                                                                                                                                                                                                                                                                                                                         AAB14150 standard; Protein; 316 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 24; 82pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYPI-) UNIV OF PITTSBURGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (YESH ) EINSTEIN A COLLEGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 aegaritglserhvvrlvaqersewleaqaarrerirayhddeghswpqtakhfglhldt 282
                                                                                                                                                                                                                                                                                                                                                                                                          283 vkrlgyrarker 294
                                                                                                                                                                                                                                                                                                                                                                                                                                       74 VH---YALNKNR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 AAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELR-SEGQSMRAIAAEVGVSVGT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
LIBRE BRUXELLES
                                                                                                                                                                                                                                                            (first entry)
                                98GB-0028217.
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                                                                99WO-EP10297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 76; DB 13; Length 314; Pred. No. 0.24; 8; Mismatches 35; Indels
                                                                                                                                                                                            factor; pathogenicity island
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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16-DEC-1999; 07-APR-2000; 03-AUG-2000;

; 99JP-0377484. ; 2000JP-0159162. ; 2000JP-0280988.

18-DEC-2000; 2000EP-0127688

20-JUN-2001 EP1108790-A2 Coryneform bacterium; amino organic acid synthesis.

acid

synthesis; vitamin;

saccharide

Corynebacterium

glutamicum

Nakagawa Tateishi

z o

Mizoguchi H, Ar Senoh A, Ikeda

Ando eda M, X

S, Hayashi M, Ozaki A;

Ochiai

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Yoko1

(KYOW) KYOWA HAKKO KOGYO

WPI; 2001-376931/40 N-PSDB; AAH66877.

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RESULT
AAG91658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bordetella pertussis possesses a type III secretion system. Type III secretion systems allow bacteria to target virulence factors directly at host cells. The present sequence is a protein of B. pertussis. No name has been specified for the present sequence. The coding sequence of the present sequence is homologous to housekeeping genes of other species, and so the present protein may have a role in cellular housekeeping. A pathogenicity island is a compact, distinct genetic unit carrying virulence genes. The coding sequence of the present sequence is located within a pathogenicity island (see AAA64890) which also carries, a number of genes encoding proteins involved in the type III secretion system of B. pertussis. See AAA64894-A64884 and AAB14111-B14146 for details of the coding sequences and proteins identified in the pathogenicity island, of the present invention.
                                                                                                                                                                                                                                                                                                 C glutamicum protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptides derived from Bordetella pertussis, useful treating and diagnosing Bordetella infection -
                                                                                                                                                                                                                                                                                                                                                                               AAG91658 standard; Protein; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Pages 160-161; 165pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-452178/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bollen
                                                                                                                                                                                                                                                                                                                           26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                     AAG91658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
                                                                                                                                                                                                                                                                                                                                                                                                                                             88 tqariaqalgvsastvsrvl 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 IAAAAKKLGVSESTVKRW-----TSEPREEFVARVAARHARIRELRSEGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vpeaaraygvtaptvrkwlgrflagggagladassrptvspraiapakalaivelrrkrl 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMRAIAAEVGVSVGTVHYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.5%;
                                                                                                                                                                                                                                                                                                 fragment SEQ.ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 69.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                 5412.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
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Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a care

oint of a gene, measuring expression of a gene, analysing profile or pattern of a gene and identifying homologous gene

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RESULT
AAU44478
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU44478 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression
         Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                               SAPHO syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                     Skeiky YAW,
                                                                                                                                                                           07-JUL-2000;
                                                                                                                                                                                      21-APR-2000;
02-JUN-2000;
                                                                                                                                                                                                                              20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                         01-NOV-2001
                                                                                                                                                                                                                                                                                   WO200181581-A2
                                                                                                                                                                                                                                                                                                               Propionibacterium
                                                                                                                                                                                                                                                                                                                                        dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes immunogenic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                        27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU44478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                               N-PSDB;
                                                                                                       L'maisonneuve J,
                                                                                                                                               (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                     inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
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                                                               2001-616774/71.
DB; AAS59522.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                    endophthalmitis; bone; joint; central nervous system; ELISA;
tory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO: 5412; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86
                                                                                                                                                                       ; 2000US-199047P.
; 2000US-208841P.
; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                    Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                       osteopathic;
                                                                                                                                                                                                                                                                                                                                                                               synovitis; acne;
                                                                                                       Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.0%;
31.6%;
                                                                                                       ۲,
                                                                                                      Mitcham JL, Wang SS,
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 67;
Pred. No.
                                                                                                                                                                                                                                                                                                                                       neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                               pustulosis; hypertosis; osteomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                           #5374.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6;
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AAE10133
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В
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Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                              16-AUG-2001
                                                                                                                                                                   Doma in
                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                        Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces noursei nystatin gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE10133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE10133 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID No 5673; 1069pp;
                                                            WO200159126-A2
                                                                                                                                                                                                                                                                                                                                                    Polyketide
                                                                                                                                                                                                                                                                                                                                                                                                                29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 gmatsmvtggtsgigrefvtqlaargddivivardtermaaikadvearygvsvetiaad 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 LNK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVSESTVKRWTSEPREEFVARVAARHARIRELRSEGQSMRAIAAEV----GVSVGTVHYA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lsr 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU39105-AAU68017 represent Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                 synthase; PKS; macrolide; nystatin; PKS gene cluster;
                                                                                                                                                                                                                                                                                                                                      antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                      /label= TM2
/note= "Transmembrane
884..912
                                                                                                                                                                                                               /note= "Leucine 548..568
                                                                                                                                                                 583..610
                                                                                                                                                                               /label= TM1
/note= "Transmembrane domain"
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                     'note= "LuxR-type helix-turn-helix motif (DNA binding)"
                                                                                                                                                                                                                                             /label- LZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.0%; Score 67; 36.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                    transcriptional activator
                                                                                                          HTH
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                                                                                                                                                                                                                            zipper motif"
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                                                                                                                                                                                                                                                                                                                                                                               NysR3
                                                                                                                                     domain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
2.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 279;
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are used in
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08-FEB-2001; 2001WO-GB00509

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ID XXX AC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
AAU59374
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Best Local S
Matches 26
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10-APR-2000;
14-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the cloning and sequencing of the cluster encoding a modular type I polyketide synthase (PKS) enzyme involved in the biosynthesis of the macrolide antibiotic nystatin. The nystatin PKS is useful as antifungal antibiotics. The present sequence is a transcriptional activator encoding Streptomyces nour.
                                                                   01-NOV-2001
                                                                                                                                                                                                         dermatological;
                                                                                                                                                                                                                       SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU59374 standard; Protein; 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYNO-)
(SNTF)
                   20-APR-2001; 2001WO-US12865
                                                                                                                                                           Propionibacterium 

                                                                                                                                                                                                                                                                                                                                                                       27-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Page 177-178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful
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(FJAE/)
                                                                                                                                                                                                                                                                                                                       Propionibacterium acnes immunogenic protein #20270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nystatin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gltnqaiatelgvs----sravekhltsa 908
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S, Ellingsen 7
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SEKUROVA O N.
FJAERVIK E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SINVENT AS.
DZIEGLEWSKA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALPHARMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene, NysR3.
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antibiotics and antifungals -
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2000GB-0008786.
2000GB-0009387.
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                                                                                                                                                                                                      osteopathic;
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Pred. No. 14;
                                                                                                                                                                                                         neuroprotectant.
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AAU58347
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CP P. acnes is also involved in infections of bone, joints and the ophthalmitis. The control of the central control of central control of the central co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 24
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02-JUN-2000;
07-JUL-2000;
                                                                                                        SAPHO syndrome; synovitis; acne; uveitis; endophthalmitis; bone; inflammatory lesion; acne vulgari
                                                                                                                                                                                            Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                          AAU58347;
                                                                                                                                                                                                                                                                                                                                    AAU58347 standard; Protein; 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequences AAU39105-AAU68017 represent Propionibacterium acnes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L'maisonneuve
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                                                                                                                                                                                                                                                                                                                                                                                                                                               85 lssnpq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRSEGQ 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt trsrkprspshglaslftmaklgvptssvpesetpkrwttspstshtaltnhadtaklfd}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YAW,
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; 2000US-208841P.
; 2000US-216747P.
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e J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The proteins and their associated DNA sequences are used by prevention and diagnosis of medical conditions caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No 20569; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 66; [Pred. No. 2
                                                                                                                           pustulosis; hypertosis; osteomyelitis;
joint; central nervous system; ELISA;
                                                                                                                                                                                                                                                                                                                                    A
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, Carter D;
                                                                                                                                                                                            protein #19243.
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Propionibacterium dermatological;

acnes

lesion; acne vulgaris; enzyme linked

immunosorbent assay;

osteopathic; neuroprotectant.

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ABB64106
ID ABB6
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AC ABB6
AC ABB6
DT 26-A
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                                                                                                                                                                                                     RESULT 13
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Best Local S
Matches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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               pharmaceutical
                               Drosophila; developmental biology; cell signalling; insecticide;
                                                               Drosophila melanogaster polypeptide SEQ ID NO 19110
                                                                                                                                                                      ABB64106 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
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                                                                                                                                                                                                                                                                                                                                                      9 RNGYSIAAAAKKLGVSESTVKRWTSEPREEFVARVAA--------
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                                                                                                                                                                                                                                                       rereilrlaesgasisliaselclsvgtvrnhvssaigktgaanrtea 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e linked immunosorbent assay (ELISA).
The sequence data for this patent did not form floation, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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28.7%;
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, Jen S, Carter
                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                      868
                                                                                                                                                                                                                                                                                                                                                                                                        Score 65.5;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
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The segmence of the invention of the segmence of the segmence of the invention o
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                                                                                                                                                                                             SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 19110; 21pp + Sequence Listing; English.
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11-JUL-2000; 2000US-0614150
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                                                                                                                     Propionibacterium acnes
                                                                                                                                                                       dermatological;
                                                                                                                                                                                                                                                                                                  Propionibacterium acnes immunogenic protein #17620
                                                                                                                                                                                                                                                                                                                                                                                                          AAU56724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU56724 standard; Protein; 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 IAAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELRSEGQSMRAIAA -- EVGVSV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                       osteopathic;
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Pred. No. 23;
15; Mismatches
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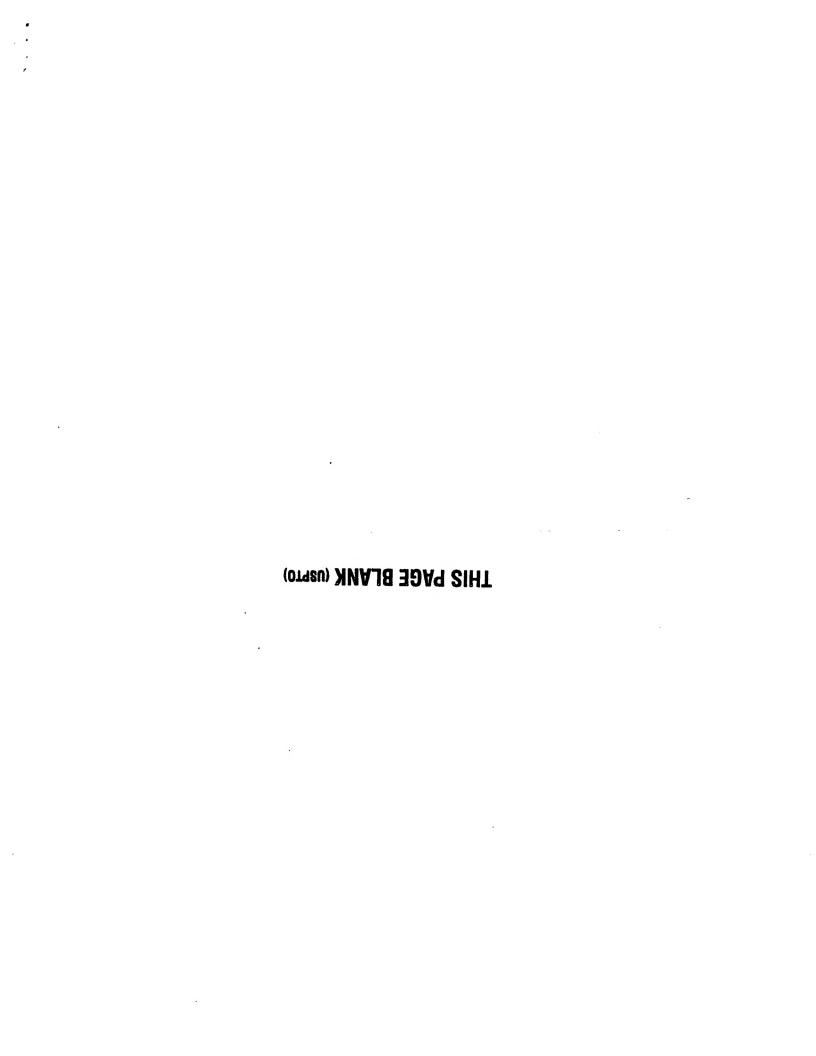
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ABB68417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyvlitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to therefore treat P. acnes infections. The antibodies can be used as diagnostic agents for determining P. acnes presence, for example, by more linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO cat fire. in the proposition of the printed specification, but was obtained in electronic format directly from WIPO cat fire. in the proposition of the printed specification, but was obtained in electronic format directly from WIPO cat fire. in the proposition of the printed specification, but was obtained in electronic format directly from WIPO cat fire.
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02-JUN-2000;
07-JUL-2000;
23-MAR-2001;
                                    27-SEP-2001
                                                                       WO200171042-A2
                                                                                                            Drosophila melanogaster
                                                                                                                                              pharmaceutical.
                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 32043
                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                   ABB68417 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAU39105-AAU68017 represent Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID No 17919; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L'maisonneuve
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                                                                                                                                                                                                                                                                                                                                                                                                          31 hrvsdvaallgvsddtvrrwldq-----rhvraakdttgrlrvdgaslaa 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 YSIAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRE-----LRSEGQSMRA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 17; Conserv
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; 2000US-208841P.
; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
2001WO-US09231
                                                                                                                                                                                                                                         (first entry)
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e J, Zhang '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-US12865
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  Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 64; DB 22;
Pred. No. 3.5;
9; Mismatches 14
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are used in
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Job time: 94 sec
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                            capable of detecting 1000 or more genes from Drosophila. The inventue useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention
                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
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11-JUL-2000;
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                                                                           16 ltprdkihaiqrihdgeskasvardigvpestlrgwcknedklrfmsrqsa 66
                                                                                           1 MTTRERLP----RNGYSIAAAAKKLGVSESTVKRW-TSEPREEFVARVAA 45 : | : : : : | : | : | : | : | : | : |
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DB; ABL12520.
                                                                                                                                                                                                                    743 AA;
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ilarity 31.4%;
Conservative 1
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2000US-0614150.
                October
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                4, 2002, 15:34:41
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                                                                                                                                                    Score 64;
Pred. No.
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25;
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and cell-cell
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
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Perfect score:
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    No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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Gapop 10.0 , Gapext 0.5
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u	44	43	42	41	40	39	38	37	36	35	34	<u>3</u> 3	32	31	30
70	70	70	70	70	70	70	70	70	70	70	70	70	70	70	70
16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7
340	340	340	340	340	340	340	340	340	340	340	340	340	340	340	340
Ν	N	N	N	N	2	N	N	N	Ŋ	N	N	N	N	N	N
AE0292	AE0254	AE0163	AE0113	AD0457	AD0417	AD0206	AD0185	AD0139	AD0124	AD0070	AC0342	AC0247	AC0031	AB0488	AB0395
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ALIGNMENTS

RESULT 2 ACC2478 ACC2478 ACC2478 C;Species: Anabaena sp. (strain PCC 7120) plasmid pCC7120alpha C;Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C;Accession: Ac2478 R;Raneko, T; Nakamura, Y; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Accession: Ac2478 A;Stratus: preliminary A;Molecule type: DNA A;Residues: 1-198 A;Cross-references: GB:BA000020; PIDN:BAB78087.1; PID:g17135541; GSPDB:GN00180 A;Experimental source: strain PCC 7120 C;Genetics:	Query Match 51.2%; Score 215; DB 2; Length 105; Best Local Similarity 53.3%; Pred. No. 7.8e-15; Matches 40; Conservative 17; Mismatches 18; Indels 0; Gaps 0; Qy 1 MTTRERLPRNGYSIAAAAKKLGVSESTVKRWTSEDREEFVARVAARHARIRELRSEGQSM 60	RESULT 1 \$32702 hypothetical protein 4 - Corynebacterium glutamicum C;Species: Corynebacterium glutamicum C;Species: Corynebacterium glutamicum C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Jun-2000 C;Accession: \$32702; \$32200 R;Shi, S.L.; Mang, Z.X.; Deng, Y.; Zhu, H.; He, B.; Zheng, Z.X. submitted to the EMBL Data Library, March 1993 A;Description: Complete nucleotide sequence of a plasmid pXZ10142 from Corynebacteriu A;Reference number: \$32699 A;Accession: \$32702 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-105 <shi> A;Cross-references: EMBL:X72691 C;Genetics: A;Start codon: GTG C;Superfamily: Corynebacterium glutamicum hypothetical protein 4</shi>

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C;Accession: D90190

R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ng arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001

A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                         hypothetical protein SS00454 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Genome: plasmid
C;Keywords: tandem repeat
F;2-13/Region: 4-residue repeats
F;75-91/Region: helix-turn-helix
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C; Comment: This protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Complete nucleotide sequence of pAL5000, a plasmid A; Reference number: JS0052; MUID:89138007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Rauzier, J.; Moniz-P
Gene 71, 315-321, 1988
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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1993
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A;Genome: plasmid
A;Cross-references: GB:AE006641; NID:gl3813609;
                   A; Molecule type: DNA
A; Residues: 1-150 <KUR>
                                                                         A; Reference number: A99139
A; Accession: D90190
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                                                        A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    AEGARITGLSERHVVRLVAQERSEWLAEQAARRERIRAYHDDEGHSWPQTAKHFGLHLDT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELR-SEGQSMRAIAAEVGVSVGT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNLSMIAEANKSPV----VPRFPQNTSLKRKVQSAKAQARRRDIHARVWSLRSIGLSVQA 75
                                                                                                                                                                                                                                                                                                                                                                                                 VH---YALNKNR 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAQSLGVAKNTVYNYLRSS 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 19.5%;
l Similarity 36.1%;
26; Conservative
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                                                                                                                                                                                                                                                                                                                                                              99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 82.5; DB 2;
; Pred. No. 0.39;
11; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (S-D-G-Y)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 82; DB Pred. No. 0.26 8; Mismatches
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 PIDN:AAK40779.1; GSPDB:GN00155
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yoc, H.P.; Redder,
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Query Match

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Score

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Length 150;

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-314 <ROM>
                                                                                                                                                                                                                                                                                                                                                          C;Species: Sphingomonas aromaticivorans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Jun-2000
C;Accession: T31220; T31222; T31221
                                                    A; Molecule type: DNA
                                                                                                   A; Accession: T31222
                                                                                                                        A; Cross-references: EMBL: AF079317; NID: g3378261; PID: g3378363; PIDN: AAD03946.1
                                                                                                                                                                                                                                 A; Reference number: A; Accession: T31220
                                                                                                                                                                                                                                                                              R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W. submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas arom
                                                                                                                                                                                                                                                                                                                                                                                                                                      transposase homolog - Sphingomonas aromaticivorans plasmid pNL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-318 <OLI>
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A; Accession: T36991
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R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, August 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL:AL031035; PIDN:CAA19911.1; GSPDB:GN00070; SCOEDB:SC6A9.26
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A;Accession: T35457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: T35457; T36991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Streptomyces coelicolor
C; Date: 05-Nov-1999 #sequence_revision
A;Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378362; PIDN:AAD03945.1
                            A; Residues: 158-314 < RO2>
                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local S
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;Gene: SCOEDB:SC6A9.26; SCOEDB:SCJ11.20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 ----EEFVARVAARHARIRELRSEGQSMRAIAAEVGVSVGTVHYAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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7; Mismatches
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1; Mismatches
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July 1998
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low affinity penicillin-binding protein 5 (PBP5) - Enterococcus C;Specias: Enterococcus faecium C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change C;Accession: S54178 R;Zorzi, W.; Zhou, X.Y.; Raze, D.; Gutmann, L.; Lamotte, J.; Dar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transposase BMEI1423 [imported]
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revi
C;Accession: AI3429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-115,145-146,'AMLSSRTVP',156,'S' <RO3>
A; Cross-references: EMBL: AF079317; NID: g3378261; PII
C: Genetics:
                                                                                      R; Zorzi, W.; Zhou, X.Y.; Raze, D.; submitted to the EMBL Data Library, A; Description: The low affinity pen
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten A;Reference number: AD3252; PMID:11756688
A;Accession: AI3429
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-674 <ZO
                                                  A; Reference number: S54175
A; Accession: S54178
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A; Introns: 115/3
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A; Status: pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: AEO08917; PIDN: AAL52604.1; PID: g17983423; GSPDB: GN00190
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Best Local S
Matches 28
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Best Local Similarity
Matches 28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                      AAAAKKLGVSESTVKRWTSEPREEFVARVAARHA----
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                                                                                                         X.Y.; Raze, D.; Gutmann, L.; Lamotte, MBL Data Library, February 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.7%;
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                                                                                      penicillin-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 74.5; DE Pred. No. 2.8; 7; Mismatches
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lzer, P.H.; Hagius, S.; O'Callaghan,
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                                                                                    protein 5
                                                                                                                                                                                                Enterococcus faecium (fragment)
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C;Genetics:
A;Gene: PAB2413
C;Superfamily: P
                                                                                                                                                                          A;Description: Pyrococcus abyssi genome
A;Reference number: A75001
A;Accession: B75055
                                                                                                                                                                                                                                                         hypothetical protein PAB1429 - Pyrococcus abyssi (strain C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_C;Accession: B75055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein PAB2413 - Pyrococcus abyssi (strain Orsay) C;Species: Pyrococcus abyssi C;Cate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change C;Accession: H75179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X84862; NID:g790432; PIDN:CAA59289.1; PID:g790433 C;Superfamily: penicillin-binding protein 2B
                                                                 C;Genetics:
A;Gene: PAB1429
                                                                                                                                                                                                                        R; anonymous, Genoscope submitted to the EMBL Data Library, July 1999
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A;Residues: 1-139 <KAW>
A;Residues: 1-139 <KAW>
A;Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB49519.1;
A;Experimental source: strain Orsay
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submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome seque
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                                                                                             A;Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50335.1; A;Experimental source: strain Orsay
                                                                                                                               A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-643 <KAW>
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A; Accession: H75179
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKVSKKVLRALEQMGIKVIPVEKGRGRPRKYSYKTL---
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17; Conserv
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19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pyrococcus abyssi hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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23.3%;
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No. 13;
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A;Residues: 1-673 <ZOR>
A;Cross-references: EMBL:X84861; NID:9790436;
C;Superfamily: penicillin-binding protein 2B
                                                                                                                                                                                                                                                                                                                                             R;Zorzi, W.; Zhou, X.Y.; Raze, D.; Gutmann, L.; Lamotte, J.; Dardenne submitted to the EMBL Data Library, February 1995
A;Description: The low affinity penicillin-binding protein 5 in wild
                                                                                                                                                                                                                                                                                                                                                                                                             low affinity penicillin-binding protein 5 (PBP5) - Enterococcus faecium (fragment) C;Species: Enterococcus faecium C;Date: 08-Jul:1995 #sequence_revision 03-Aug-1995 #text_change 26-May-2000
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A; Description: The low affinity penicillin-binding protein 5 in wild ty
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A; Accession: S54182
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A; Residues: 1-673 < ZOR>
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A; Accession: S54175
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                                                                   PKTGDLLALASSPSYDPNKMTNGISQEDYKSYEENPEQPFISRFATGYA-----PGST 418
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19; Conser
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16; Mismatches
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Pred. No. 14;
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probable IS1617 transposase - Yersinia pestis plasmid pCD1
C;Species: Yersinia pestis
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T43610; T42913
R;Hu, P.; Elliott, J.; McCready, P.; Skowronski, F. Carron T. T.
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A36903
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A;Experimental source: S185
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A;Title: Cloning and sequencing of the low-affinity penicillin-binding protein 3r-enc A;Reference number: A36903; MUID:93259926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          low-affinity penicillin-binding protein 3r - Enterococcus hirae C;Species: Enterococcus hirae C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
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A;Molecule type: DNA
A;Residues: 1-678 <ZOR>
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R; Zorzi, W.;
                                                                                                                                         RESULT 15
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A; Residues: 1-678 <PIR>
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16; Mismatches
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J. Bacteriol. 180, 5192-5202, 1998
A;Title: Structural organization of virulence-associated plasmids of Yersinia pestis.
A;Reference number: Z22578; MUID:98422474
A;Reference number: Z22578; MUID:98422474
A;Reference number: Z43610
A;Ccossion: T43610
A;Ccossion: Teplininary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-88 < HUPA
A;Cross-references: EMBL.AF053946; NID:92996222; PIDN:AAC62592.1; PID:92996269
A;Experimental source: Strain KIM
R;Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R.
Infect. Immun. 66, 4611-4623, 1998
A;Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia
A;Reference number: Z2273; MUID:98427122
A;Accession: T42913
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-88 < PER-
A;Cross-references: EMBL:AF074612; NID:93822037; PIDN:AAC69821.1; PID:93822101
A;Experimental source: Strain KIM5
C;Genetics:
A;Genome: plasmid pCD1
A;Experimental source: Strain KIM5
D;Genetics:
A;Genome: plasmid pCD1
A;Experimental source: Strain KIM5
C;Genetics:
A;Genome: plasmid pCD1
A;Experimental source: Strain KIM5
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ILEU_PIG
MAPB_HUMAN
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TODA_PSEPU
                                                                                         ALFB_RABIT
ALFB_RAT
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P23071 myxococcus
083057 treponema p
P39212 escherichia
075679 escherichia
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sus scrofa
homo sapien
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escherichia
                                                                   salmonella
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saccharomyc
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RESULT 2 RT65_MYXXA ID RT65_MYXXA AC P23071: DT 01-NOV-1991 01-NOV-1991 01-NOV-1991 01-NOV-1991 01-NOV-1998 015-DEC-1998 0

STANDARD;

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(Rel. 20, Created)
(Rel. 20, Last sequence update)
(Rel. 37, Last annotation update)

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y 34. y 34. rvative sestvkr : L: slstmtr		Froteobacteria; F622; F622; FROM N.A. C 11546; C 11546; C 19839; PubMed- C 299839; PubMed- C C 15911. C 172:4090-40 C I 172:4090-40 C I 1911. C I SBILONGS T	STANDARD; L. 31, Cr l. 31, La l. 31, La N for ins	100 301 308 462 848 879 880 232 232 232 2312 414
O#;	inspending Manual Manua	1; 9; he 100 100 100 100 100 100 100 100 100 10	RD; Created) Last seq Last ann	
al Similarity 34.0%; pred. No. 0.7 18; Conservative 9; Mismatches YSIAAAAKKLGVSESTVKRWTSEPREEFVAR :: : : : YTVADAAKAMDVGLSTMTRWVKQLRDERQGKTPKASP	Swiss Institute of Bioinform Bioinformatics Institute. T profit institutions as long this statement is not remove ires a license agreement (Se ail to license@isb-sib.ch). NOT_ANNOTATED_CDS. (202514; Transposase_8.); Transposase_8.); Transposase_8. Plansposase_8.7 element; Transposition; DNA- 2 AA; 12739 MW; 7B01B52B5E		ALIGI PRT; uence otation	YIS1_SHISO YWBI_BACSU LLIPA_CHLMU REGB_RHOSH MYSP_DIRIN MYSP_ONCVO WYSP_BRUMA YAGI_ECOLI YG17_HSVI1 YM82_MYCTU YM42_MYCTU YM42_MYCTU YM42_ARATH
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Y013_TREPA
O83057;
15-DEC-1998
                                                                               Treponema pallidum.
Bacteria; Spirochaetales;
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15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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STRAIN-NICHOLS;
MEDLINE-98332770; PubMed-9665876;
Fraser C.M., Norris S.J., Weinsto
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0866; RNADNAPOLMS.
Transferase; RNA-directed RNA
SEQUENCE 427 AA; 48024 MW;
                                          SEQUENCE FROM N.A.
                                                                   NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00078; rvt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A34864; RRYC65.
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OC. NATI. ACAD. SCI. U.S.A. 87:942-945(1990).

- FUNCTION: PARTICIPATES IN THE SYNTHESIS OF A MSDNA (A BRANCHED I LINKED BY A 2',5'-PHOSPHODIESTER LINKAGE TO A SINGLE-STRANDED DI OF UNKNOWN FUNCTION. THE RETRON TRANSCRIPT SERVES AS PRIMER AND TEMPLATE TO THE REACTION, AND CODES FOR THE RT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: RETRONS
SIMILARITY: TO OTHER RE
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S., Herzer P.J., Inouye M.;
                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000123;
IPR000477;
                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 4.6;
13; Mismatches
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Matches 19
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P39212;
01-FEB-1995 (Rel.
01-FEB-1995 (Rel.
16-OCT-2001 (Rel.
            EcoGene; EG40014; insN.
InterPro; IPR002514; Transposase_8.
Pfam; PF01527; Transposase_8; 1.
                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                         "Analysis of the Escherichia coli genome VI: DNA region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                              STRAIN-K12 / MG1655;
MEDLINE-95334362; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical SEQUENCE 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@isb-slb.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weldman J., Smith H.O.,
                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                           Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                     Burland V.D., Plunkett
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter J.C.
                                                          EMBL; AE000499; AAC77239.1;
                                                                        EMBL; U14003; AAA97179.1;
                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE TRANSPOSASE FAMILY 8.
                                                                                                                                                                                                                                                                                                                       Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
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                                                                                                                                                                                                                                            SEQUENCE IS911.
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19; Conserv
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nilarity 32.2%;
Conservative
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Hardham
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for insertion sequence element
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McLeod M.P., S
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5E1B311377B49DB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             subdivision; Enterobacteriaceae;
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                                                                                                                    http://www.isb-sib.ch/announce/
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element;

Transposition;

DNA-binding; DNA recombination;

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Davis R.W.;
Submitted (SEP-1996) to the
Submitted INVOLVED IN TH
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the Euro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blatther F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                       EMBL; AE000133; AAC73358.1; -.
EMBL; D83536; BAA77925.1; -.
EMBL; U70214; AAB08674.1; ALT_INIT.
ECOGENE; EG40014; InsN.
InterPro; IPR002514; Transposase_8; 1.
Pfam; PF01527; Transposase_8; 1.
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16-OCT-2001 (Rel. 40, Last sequ
01-MAR-2002 (Rel. 41, Last anno
Transposase insN for insertion
                                                                                                                                           entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                         use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                  Schramm S., Duncan M.
Davis K., Federspiel
Lashkari D., Lew H.,
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P75679; P71288;
                         Transposable element; Transposition; DNA-binding; DNA recombination;
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European Bioinformatics Institute.
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134 AA;
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32.1%;
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Lin D., Namath A., Oefner P., Roberts D.,
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BF1A0B16CB666AF3 CRC64;
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Matches

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014301;
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                                                                                                                                                                                                                                                                                                                                                                          Churcher C.M., Gentles S., Barrell B.G., Rajandream M.A., Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases. -!- SIMILARITY: CONTAINS 11 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998
16-OCT-2001
                                                                                  REPEAT
REPEAT
                                                                                                                           REPEAT
REPEAT
                                                                                                                                                                                      PROSITE; PS00678; WD_REPEATS_1; FALSE_N PROSITE; PS50082; WD_REPEATS_2; 6. PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                 entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomycetales; Schizosaccharomyces.
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                                                              REPEAT
                                                                                                                                                REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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32.1%;
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Score 67.5; I
Pred. No. 15;
L4; Mismatches
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Pred. No. 2
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Q28634;
16-OCT-2001
16-OCT-2001
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Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cramania: Entheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     member of the cadherin multigene fami
J. Biol. Chem. 270:17594-17601(1995)
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
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DOMAIN
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Pfam; PF00028; cadherin; 6.
SMART; SM00112; CA; 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation and cDNA cloning of Ksp-cadherin, member of the cadherin multigene family.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95340560; PubMed=7615566;
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                                                                                                                                                                                                                        PROSITE; PS00232; CADHERIN_1; 2. PROSITE; PS50268; CADHERIN_2; 6.
                                                                                              DOMAIN
                                                                                                                                                                                                              Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                              BIOI. Chem. 270:17594-17601(1995).

BIOI. Chem. 270:17594-17601(1995).

FUNCTION: CADHERINS ARE CALCUUM DEPENDENT CELL
THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN
MANUER IN CONNECTING CELLS; CADHERINS MAY THUS
SORTING OF HETEROGENEOUS CELL TYPES.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: KIDNEY-SPECIFICAL LIMITED TO
MEMBRANES OF RENAL TUBULAR EPITHELIAL CELLS.

MEMBRANES OF RENAL TUBULAR EPITHELIAL CELLS.
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Last annotation updat
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Best Local
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Berardini T.Z., Amsden A.B., Penhoet E.E., Tolan D.R.;

Berardini T.Z., Amsden A.B., Penhoet E.E., Tolan D.R.;

Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

-I- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone

phosphate + D-glyceraldehyde 3-phosphate.

-I- PATHWAY: SIXHH STEP IN GLYCOLYSIS.

-I- PATHWAY: SIXHH STEP IN GLYCOLYSIS.

-I- SUBUNIT: HOMOTETRAMER.

-I- SUBUNIT: HOM
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BINDING
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Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
Fructose-bisphosphate aldolase B (EC '
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Mammalia; Eutheria; Lagomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
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PS00158; ALDOLASE_CLASS_I; 1.
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0 BY SIMILARITY.

55 C-1-PHOSPHATE GROUP OF THE SUBSTRATE.

146 C-1-PHOSPHATE GROUP OF THE SUBSTRATE.

229 SCHIFF-BASE WITH DIHYDROXYACETONE-P.
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                                                                                                                                                                                                                                                                                                                                                                     ESSENTIAL FOR ENHANCED ACTIVITY OF THE ENZYME TOWARD FRUCTOSE 1,6-BISPHOSPHATE AS COMPARED WITH FRUCTOSE 1-PHOSPHATE. 0A7185A72E89F436 CRC64;
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4.1.2.13) (Liver-type aldolase).
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RESULT
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J. Biol. Chem. 258:6537-6542(1983).
J. Biol. Chem. 258:6537-6542(1983).
III. Chem. 258:6537-6542(1983).
III. Chem. 258:6537-6542(1983).
III. Chem. 258:6537-6542(1983).
III. CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glyophosphate.
III. PATHWAY: SIXTH STEP IN GLYCOLYSIS.
III. SUBUNIT: HOMOTETRAMER.
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21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
Fructose-bisphosphate aldolase B (EC 4.1.2.
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Yatsuki H., Hori K., Ishikawa K.;
"Nucleotide sequence of rat liver aldolase
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T Sutsumi R.,
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Mammalia; Eutheria;
  PROSITE;
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SL; X02284; CAA26156.1; -

SL; X02285; CAA26156.1; J

SL; X02287; CAA26156.1; J

SL; X02288; CAA26156.1; J

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by non-profit institutions as lon lifted and this statement is not remove. It requires a license agreement (Seend an email to license@isb-sib.ch).
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PPRO; IPR000741; Aldolase_I.
PF00274; 9lycolytic_enzy; 1.
m; PD001128; Aldolase_I; 1.
TE; PS00158; ALDOLASE_CLASS_I;
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RESULT 10
MOES_LYTVA
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                                                                                                                                                                                                                                                                           Bachman E.S., McClay D.R.;
"Characterization of moesin in the sea urchin Lytechinus variegatus:
redistribution to the plasma membrane following fertilization is
inhibited by cytochalasin B.";
J. Cell Sci. 108:161-171(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-95256329;
           Structural protein; Cy
DOMAIN 58 224
                              PROSITE; PS00660; BAND_41_1;
PROSITE; PS00661; BAND_41_2;
PROSITE; PS50057; BAND_41_3;
                                                               Pfam; PF00769; ERM; 1. PRINTS; PR00935; BAND41. SMART; SM00295; B41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            Moesin.
                                                                                                                                 EMBL; U14180; AAC46514.1;
                                                                                                                                                                                                                                                                                                                                                                                         Echinoidea;
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                                                                                                            InterPro;
                                                                                                                       InterPro; IPR000299;
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                                                                                                 PF00373; Band_41;
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Echinodermata; Eleutherozoa; Echinozoa;
oidea; Echinacea; Temnopleurolda; Toxopneustidae;
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                   Cytoskeleton
67579 MW;
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25.6%;
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C-1-PHOSPHATE GROUP OF THE SUBSTRATE.
SCHIEF-BASE WITH DIHYDROXYACETONE-P.
ESSENTIAL FOR ENHANCED ACTIVITY OF THE
ENZYME TOWARD FRUCTOSE 1,6-BISPHOSPHATE
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ced. No. 13;
Mismatches
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8EF4F3E621E6DD9A
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            4.1-LIKE
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Best Local Similarity
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EMBL; AE000428; AAC76545.1; -.
HSSP; P10957; IRNL.
ECOGene; EG12246; yhjB.
InterPro; IPR000792; HTH_LuxR.
Pfam; PF00196; GerE; 1.
PRINTS; PR00038; HTHLUXR.
SMART; SM00421; HTH_LUXR; 1.
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P37640;
01-OCT-1994
01-OCT-1994
16-OCT-2001
                                                                                                                                                     Hypotheticar Formation 159 178 H. The Tring 159 178 H. The Tring 159 AA; 22604 MW;
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Hypothetical protein; Transcription regulation; DNA-binding;
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                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for conmodified
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MEDLINE-94316500; PubMed-8041620;
Sofia H.J., Burland V., Daniels D.L.,
Sofia H.J., Burland V., Daniels D.L.,
Panalysis of the Escherichia coli genc
region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994)
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NRTQA 192
                       NRTDA 85
                                               WRTTPEKDIKDLKSLSARQREILTMLAAGESNKEIGRALNISTGTVKAHLESLYRRLEVK 187
                                                                       WTSEPREEF -- VARVAARHARIRELRSEGQSMRAIAAEVGVSVGTVHYALN------
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27.7%;
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29.9%;
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Pred. No.
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RESULT 12
ATCU_RHIME
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Pfam; PF00403; HMA; 2.

Pfam; PF00702; Hydrolase; 1.

PF1NTS; PR00119; CATATPASE.

PRINTS; PR00940; CATPATPASEA.

PRINTS; PR00941; CDATPASEA.

PRINTS; PR00941; CDATPASE

PRINTS; PR00946; HGSCAVENGER.

PROSITE; PS00154; ATPASE_E1_E2; 1.

PROSITE; PS01047; HMA_1; 2.

PROSITE; PS01047; HMA_2; 2.

Hydrolase; Transmembrane; Phosphorylation; Marketal.
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TRANSMEM 174
TRANSMEM 210
TRANSMEM 248
TRANSMEM 271
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Q9XSX3;

Q9XSX3;

30-MAY-2000 (Rel. 39, Created)

30-MAY-2000 (Rel. 39, Last seq

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            TRANSMEM
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"The role of copper and P-type ATPase in the acid-tolerance of
Rhizobium leguminosarum by viciae and Sinorhizobium meliloti.",
Submitted (FEB-199) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN COPPER TRANSPORT (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + H(2)0 - ADP + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF129004; AAD27639.1; -. HSSP; Q04656; 1AW0.
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-!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPA
(E1-E2 ATPASES). SUBPAMILY IB.
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IPR000579; Cat_P_ATPas
IPR001757; E1-E2_ATPas
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 Cat_P_ATPaseA.
E1-E2_ATPase.
HG_scavenger.
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RESULT 14
ALFB_SHEEP
ID ALFB_S
AC P52210
DT 01-OCT
DT 01-OCT
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Best Local :
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Best Local :
                                                                                                                                                  Matches
 P52210;
01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 18.1 kDa protein in MDS3-GCN1 intergenic region.
YGL196W OR G1315.
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METAL
                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97197971; PubMed=9046087; Coglievina M., Klima R., Bertani
                                      ALFB_SHEEP
                                                                                                                                                                                                             Hypothetical protein. SEQUENCE 165 AA; ]
                                                                                                                                                                                                                                             EMBL; Z72718; CAA96908.1; -.
EMBL; X91837; CAA62948.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                 Yeast 13:55-64(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequencing of a 40.5 kb fragment located on chromosome VII from Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-S288C / FYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                   112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGU6_YEAST
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                                                                                                                        3 TRERLPRNGYSIAAAAKKLGVSESTVKRWTSEPREEFVARVAARHARIRELRS 55
                                                                                                                                                                                                                                                                                                                                                                                      FRAMESHIFT IN POSITION 148.
                                                                                                 TREASSIKGFGICADLEHVLKSESFSREW-----YVARVSQEHGILRPIRN
                                                                                                                                                                                                                                      S0003164; YGL196W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGYSIAAAKKLGVSESTVKRWTSEPREEFVARV--AARHARIRELRSEGQSMRAIA--- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRRTAEAIAKKLGI----
                                                                                                                                                 17; Conserv
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23; Conservative
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  (Rel.
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34, Last seq
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718
86239
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32.1%;
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sequence
                                                                                                                                              Score 64.5; DE Pred. No. 8; 9; Mismatches
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MAGNESIUM (BY SIMILARITY).
707E2148DDDA5004 CRC64;
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RESULT 15
ATC2_RHIME
ID ATC2_RHIME
AC P58342;
DT 01-MAR-2002
DT 01-MAR-2002
DT 01-MAR-2002
DE Copper-trans
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INIT_MET
BINDING
BINDING
BINDING
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochim. Biophys. Acta 1219:223-227(1994).

-- CATALYTIC ACTIVITY: D-fructose 1.6-bisphosphate = 9ly phosphate + D-glyceraldehyde 3-phosphate.

-- PANTWAY: SIXTH STEP IN GLYCOLYSIS.

-- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

-- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

-- MISCELLANEOUS: IN VERTEBRATES, THREE FORMS OF THIS UB GLYCOLYTIC ENZYME ARE FOUND, ALDOLASE A IN MUSCLE, AL LIVER, & ALDOLASE C IN BRAIN.

-- SIMILARITY: BELONGS TO CLASS I FRUCTOSE-BISPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00274; glycolytic_enzy; 1.
ProDom; PD001128; Aldolase_I; 1.
PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
Lyase; Schiff base; Glycolysis; Multig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a control between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z29372; CAA82563.1; HSSP; P00883; 1ADO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gianquinto Cotinot C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Mesonephros;
MEDLINE=94368863; PubMed=8086469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
Bovidae; Caprinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALDOB
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aldolase B from fetal mesonephros."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Last annotation update) Fructose-bisphosphate aldolase B (EC 4.1.2.13) (Liver-type aldolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9940;
                                                                                                                                                         78
                                                                                                                                                                                    45 ARHARIRELRSEGQSMRAIAAEVGVSVG
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                                                                                                                                                       LFHETLYQKDGQGKLFRDILKEKGIVVG
                                                                                                                                                                                                                  TARRIVANGKGILAADESVGTMGNRLQRIKVENTEENRRQFRELLFTVDSSVSQSIGGVI 77
                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L., Pailhoux E.A.,
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                                                                                                                                                                                                                                                                                                                                                          363
(Rel. 41, Created)
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(Rel. 41, Last annotation)
(Rel. 41, Tast annotation)
                                                                                                                                                                                                                                                                                                                                                                                                       55
146
229
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                                                                                                                                                                                                                                                                             Conservative
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                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                  ; Glycolysis; Multigene family.

BY SIMILARITY.

C-1-PHOSPHATE GROUP OF THE SUBSTRATE.

C-1-PHOSPHATE GROUP OF THE SUBSTRATE.

C-1-PHOSPHATE GROUP OF THE SUBSTRATE.

SCHIFF-BASE WITH DIHYDROYACETOME-P.

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                                                                                                                                                                                                                                                                             Pred. No. 20;
3; Mismatches
                                                                                                                                                                                                                                                                                                            Score
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                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                        COMPARED WITH FRUCTOSE 1-PHOSPHATE. FC8B45666821E2BD CRC64;
                                                                                                                                                                                                                                                                                            No.
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20;
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6 outstation –
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Copper-transporting

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Best Local Similarity
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SEQUENCE
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DOMAIN
METAL
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Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid psymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL603645; CAC49418.1; -. PROSITE; PS00154; ATPASE_E1_E2; 1. PROSITE; PS01047; HMA_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puehler A.;
                                                                                                                                                                          MOD_RES
                                                                                                                                                                                                METAL
METAL
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                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                               Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01047; HMA_1; 2. PROSITE; PS50846; HMA_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (E1-E2 ATPASES). SUBFAMILY IB.
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                                            670
717 NDAPALAEADVGIAVGT 733
                       65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein (By similarity). SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
                    -----AEVGVSVGT 73
                                            NRRTAEAIARKLGI-------DEVVAEVLPEGKVEAIRKLRQGGRSVAFIGDGI 716
                                                                 NGYSIAAAAKKLGVSESTVKRWTSEPREEFVARV--AARHARIRELRSEGQSMRAIA---
                                                                                            23;
                                                                                           Conservative
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771
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797
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83
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515
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478
793
819
                                                                                                                                                    85861 MW;
                                                                                                    15.2%;
                                                                                                                                                                                                                                                                                                                                                              Repeat;
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                                                                                           11; Mismatches
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COPPER (POTENTIAL).

COPPER (POTENTIAL).

COPPER (POTENTIAL).

COPPER (POTENTIAL).

COPPER (POTENTIAL).

PHOSPHORYLATION (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).
                                                                                                    Score 64; DB 1; Length 827; Pred. No. 47;
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POTENTIAL.
POTENTIAL.
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